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OM protein - protein search, using sw model

Run on: June 26, 2005, 12:10:37 ; Search time 30.1562 Seconds  
(without alignments)  
2279.856 Million cell updates/sec

Title: US-10-697-894-39  
Perfect score: 4781  
Sequence: 1 MRQPASRDLPQBPVPPG.....VPLDGRAPINGCCSLDAE 921

Scoring table: BLOSUM62  
Gapop 10.0 , Gapext 0.5

Searched: 513545 seqs, 74649064 residues

Total number of hits satisfying chosen parameters: 513545

Minimum DB seq length: 0  
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%  
Maximum Match 100%  
Listing first 45 summaries

Database : Issued Patents AA:\*  
1: /cgn2\_6/prodata/1/aaa/5A\_COMB.pep:\*  
2: /cgn2\_6/prodata/1/aaa/5B\_COMB.pep:\*  
3: /cgn2\_6/prodata/1/aaa/6A\_COMB.pep:\*  
4: /cgn2\_6/prodata/1/aaa/6B\_COMB.pep:\*  
5: /cgn2\_6/prodata/1/aaa/PCTUS\_COMB.pep:\*  
6: /cgn2\_6/prodata/1/aaa/backfiles1.pep:\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	4781	100.0	921	1 US-07-872-644-39	Sequence 39, Appl
2	4781	100.0	921	1 US-08-297-494-39	Sequence 39, Appl
3	4781	100.0	921	1 US-08-297-510-39	Sequence 39, Appl
4	4781	100.0	921	1 US-08-479-532-39	Sequence 39, Appl
5	4781	100.0	921	1 US-08-455-526-39	Sequence 39, Appl
6	4781	100.0	921	1 US-08-455-525-39	Sequence 39, Appl
7	4781	100.0	921	3 US-09-139-491-39	Sequence 39, Appl
8	4781	100.0	921	3 US-09-754-250-5	Sequence 5, Appl
9	4781	100.0	921	5 PCT-US92-03222-39	Sequence 39, Appl
10	4781	100.0	921	1 US-07-872-644-43	Sequence 43, Appl
11	4657	97.4	942	1 US-08-297-494-43	Sequence 43, Appl
12	4657	97.4	942	1 US-08-297-510-43	Sequence 43, Appl
13	4657	97.4	942	1 US-08-479-532-43	Sequence 43, Appl
14	4657	97.4	942	1 US-08-455-526-43	Sequence 43, Appl
15	4657	97.4	942	1 US-08-455-525-43	Sequence 43, Appl
16	4657	97.4	942	3 US-09-139-491-43	Sequence 43, Appl
17	4657	97.4	942	4 US-09-883-825-43	Sequence 43, Appl
18	4657	97.4	942	5 PCT-US92-03222-43	Sequence 43, Appl
19	4657	97.4	942	3 US-09-754-250-2	Sequence 2, Appl
20	4533.5	94.8	920	1 US-07-872-644-45	Sequence 45, Appl
21	4474.5	93.6	941	1 US-08-297-494-45	Sequence 45, Appl
22	4474.5	93.6	941	1 US-08-297-510-45	Sequence 45, Appl
23	4474.5	93.6	941	1 US-08-479-532-45	Sequence 45, Appl
24	4474.5	93.6	941	1 US-08-455-526-45	Sequence 45, Appl
25	4474.5	93.6	941	1 US-08-455-525-45	Sequence 45, Appl
26	4474.5	93.6	941	3 US-09-139-491-45	Sequence 45, Appl
27	4474.5	93.6	941		

28	4474.5	93.6	941	4 US-09-883-825-45	Sequence 45, Appl
29	4474.5	93.6	941	4 US-09-708-392-5	Sequence 5, Appl
30	4474.5	93.6	941	4 US-09-949-016-6244	Sequence 6244, Ap
31	4474.5	93.6	941	5 PCT-US92-03222-45	Sequence 45, Appl
32	4473.5	93.6	905	3 US-09-754-250-4	Sequence 4, Appl
33	3698	77.3	802	4 US-09-949-016-7922	Sequence 7922, Ap
34	914.5	19.1	779	3 US-08-951-648-6	Sequence 6, Appl
35	914.5	19.1	779	3 US-09-174-437-6	Sequence 6, Appl
36	914.5	19.1	779	4 US-09-686-055A-6	Sequence 1, Appl
37	914.5	19.1	779	4 US-09-420-190-1	Sequence 1, Appl
38	913	19.1	803	2 US-08-951-648-4	Sequence 4, Appl
39	913	19.1	803	3 US-09-174-437-4	Sequence 4, Appl
40	913	19.1	803	3 US-09-686-055A-4	Sequence 4, Appl
41	912.5	19.1	766	3 US-08-951-648-2	Sequence 2, Appl
42	912.5	19.1	766	3 US-09-174-437-2	Sequence 2, Appl
43	912.5	19.1	766	4 US-09-686-055A-2	Sequence 2, Appl
44	801	16.8	875	1 US-08-480-547A-23	Sequence 23, Appl
45	801	16.8	875	1 US-08-250-847B-23	Sequence 23, Appl

ALIGNMENTS

RESULT 1  
US-07-872-644-39  
; Sequence 39, Application US/07872644  
; Patent No. 5389527  
; GENERAL INFORMATION:  
; APPLICANT: Beavo, Joseph A.  
; APPLICANT: Bentley, Kelley  
; APPLICANT: Charbonneau, Harry  
; APPLICANT: Sonnenburg, William K.  
; TITLE OF INVENTION: DNA Encoding Mammalian  
; TITLE OF INVENTION: Phosphodiesterases  
; NUMBER OF SEQUENCES: 58  
; CORRESPONDENCE ADDRESS:  
; ADDRESSEE: Marshall, O'Toole, Gerstein, Murray &  
; ADDRESSEE: Bicknell  
; STREET: Two First National Plaza, 20 South Clark  
; STREET: Street  
; CITY: Chicago  
; STATE: Illinois  
; COUNTRY: USA  
; ZIP: 60603  
; COMPUTER READABLE FORM:  
; MEDIUM TYPE: Floppy disk  
; COMPUTER: IBM PC compatible  
; OPERATING SYSTEM: PC-DOS/MS-DOS  
; SOFTWARE: PatentIn Release #1.0, Version #1.25  
; CURRENT APPLICATION DATA:  
; APPLICATION NUMBER: US/07/872,644  
; FILING DATE: 19920420  
; CLASSIFICATION: 435  
; PRIOR APPLICATION DATA:  
; APPLICATION NUMBER: US 07/688,356  
; FILING DATE: 04-APR-1991  
; ATTORNEY/AGENT INFORMATION:  
; NAME: No. 5389527and, Greta E.  
; REGISTRATION NUMBER: 35,302  
; REFERENCE/DOCKET NUMBER: 27866/30822  
; TELECOMMUNICATION INFORMATION:  
; TELEPHONE: (312) 346-5750  
; TELEFAX: (312) 984-9740  
; TELEX: 25-3856  
; INFORMATION FOR SEQ ID NO: 39:  
; SEQUENCE CHARACTERISTICS:  
; LENGTH: 921 amino acids  
; TYPE: AMINO ACID  
; TOPOLOGY: linear  
; MOLECULE TYPE: protein  
US-07-872-644-39

Query Match 100.0%; Score 4781; DB 1; Length 921;

Best Local Similarity 100.0%; Pred. No. 0;			
Matches 921; Conservative 0; Mismatches 0; Indels 0; Gaps 0;			
Qy	1	MRQPAASRDIFAQEPVPPGSGDGLQDALLSLGSDVIDVAGLQQAQVKEALSAPLKVETV	60
Db	1	MRQPAASRDIFAQEPVPPGSGDGLQDALLSLGSDVIDVAGLQQAQVKEALSAPLKVETV	60
Qy	61	YTYLLDGSRLVCEPPELPOEGKVRBAVTSRKRKLCNGLGPSPDLGPKPLARLVAPLAP	120
Db	61	YTYLLDGSRLVCEPPELPOEGKVRBAVTSRKRKLCNGLGPSPDLGPKPLARLVAPLAP	120
Qy	121	DTQVLVPLVDKEGAAVAAILVHCGQLSDNEEWSLQAVEKHTLVALKRVQALQORESSV	180
Db	121	DTQVLVPLVDKEGAAVAAILVHCGQLSDNEEWSLQAVEKHTLVALKRVQALQORESSV	180
Qy	181	APATQNPPEAAGDKGGVAYTNQDKILQICGELYDLDASSILQKLVYLQOQETQASR	240
Db	181	APATQNPPEAAGDKGGVAYTNQDKILQICGELYDLDASSILQKLVYLQOQETQASR	240
Qy	241	CCLLLVSEDNILQLSCKVIGDKVLEEEISFPITTTGRLGQGVVDEKKSILQKDLTSDMQQLQ	300
Db	241	CCLLLVSEDNILQLSCKVIGDKVLEEEISFPITTTGRLGQGVVDEKKSILQKDLTSDMQQLQ	300
Qy	301	SMLGCEVQAMLCVPVISRATDQVVVALACAFNKLGGDLFTDQDEHVIQHCFTYTTVLTST	360
Db	301	SMLGCEVQAMLCVPVISRATDQVVVALACAFNKLGGDLFTDQDEHVIQHCFTYTTVLTST	360
Qy	361	LAFQKEQKLKCEQALLQVAKNLFTHLDDVSVLLQEIITEARNLSNAEICSVFLLDQNEL	420
Db	361	LAFQKEQKLKCEQALLQVAKNLFTHLDDVSVLLQEIITEARNLSNAEICSVFLLDQNEL	420
Qy	421	VAKVFDGSGVDESEYIRIPADQGIAGHVATTGQLNIPDAVAPLFRVGVDDSTGRTR	480
Db	421	VAKVFDGSGVDESEYIRIPADQGIAGHVATTGQLNIPDAVAPLFRVGVDDSTGRTR	480
Qy	481	NILCFPIKNEQVIGVLAELNKGMPFSKFDDELATAFSIYCGISIAHSLLYKKVNEA	540
Db	481	NILCFPIKNEQVIGVLAELNKGMPFSKFDDELATAFSIYCGISIAHSLLYKKVNEA	540
Qy	541	QYRSHLANEMMYHMKVSDDEYTKLLHDGIQFVAADSNFASFTYTPRSLPEDDTSMAIL	600
Db	541	QYRSHLANEMMYHMKVSDDEYTKLLHDGIQFVAADSNFASFTYTPRSLPEDDTSMAIL	600
Qy	601	SMLODMFNNYKIDCPTLAPFCLMVKGYRDPVYHNMHAFSVSHFCYLLYKNLELTNY	660
Db	601	SMLODMFNNYKIDCPTLAPFCLMVKGYRDPVYHNMHAFSVSHFCYLLYKNLELTNY	660
Qy	661	LEDMEIFALFISCMCHDLDRGTNNSFOVASKSVLAALYSSEGSMERHHPAQAIILNT	720
Db	661	LEDMEIFALFISCMCHDLDRGTNNSFOVASKSVLAALYSSEGSMERHHPAQAIILNT	720
Qy	721	HGCNIFDHFSRKDYQRMOLDLMDRIILATDLAHLRIIPKDLQMAEVGYDRTNKQHSLLL	780
Db	721	HGCNIFDHFSRKDYQRMOLDLMDRIILATDLAHLRIIPKDLQMAEVGYDRTNKQHSLLL	780
Qy	781	CLMTSCDLSQTKGKWTTRKIAELIYKEPFSQGDLEKAMGNRMENMDREKAYIPBLQI	840
Db	781	CLMTSCDLSQTKGKWTTRKIAELIYKEPFSQGDLEKAMGNRMENMDREKAYIPBLQI	840
Qy	841	SFMEHIAMPIYKLLQDLFPKAAELYERVASNREHWTKVSHKFTTIRGLPSSNLSDFLDEEY	900
Db	841	SFMEHIAMPIYKLLQDLFPKAAELYERVASNREHWTKVSHKFTTIRGLPSSNLSDFLDEEY	900
Qy	901	EVPLDGGARAPINGCCSLDAE 921	
Db	901	EVPLDGGARAPINGCCSLDAE 921	

RESULT 2  
US-08-297-494-39  
; Sequence 39, Application US/08297494  
; Patent No. 5580771  
; GENERAL INFORMATION:

APPLICANT: Beavo, Joseph A.  
APPLICANT: Bentley, Kelley  
APPLICANT: Charbonneau, Harry  
APPLICANT: Sonnenburg, William K.  
TITLE OF INVENTION: DNA Encoding Mammalian  
TITLE OF INVENTION: Phosphodiesterases  
NUMBER OF SEQUENCES: 58  
CORRESPONDENCE ADDRESS:  
ADDRESSEE: Marshall, O'Toole, Gerstein, Murray &  
ADDRESSEE: Bicknell  
STREET: Two First National Plaza, 20 South Clark  
STREET: Street  
CITY: Chicago  
STATE: Illinois  
COUNTRY: USA  
ZIP: 60603  
COMPUTER READABLE FORM:  
MEDIUM TYPE: Floppy disk  
COMPUTER: IBM PC compatible  
OPERATING SYSTEM: PC-DOS/MS-DOS  
SOFTWARE: PatentIn Release #1.0, Version #1.25  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/08/297,494  
FILING DATE:  
CLASSIFICATION: 435  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: US 07/688,356  
FILING DATE: 04-APR-1991  
ATTORNEY/AGENT INFORMATION:  
NAME: No. 5580771and, Greta E.  
REGISTRATION NUMBER: 35,302  
REFERENCE/DOCKET NUMBER: 27866/30822  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: (312) 346-5750  
TELEFAX: (312) 984-9740  
TELEX: 25-3856  
INFORMATION FOR SEQ ID NO: 39:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 921 amino acids  
TYPE: amino acid  
TOPOLOGY: linear  
MOLECULE TYPE: protein  
US-08-297-494-39

Query Match 100.0%; Score 4781; DB 1; Length 921;			
Best Local Similarity 100.0%; Pred. No. 0;			
Matches 921; Conservative 0; Mismatches 0; Indels 0; Gaps 0;			
Qy	1	MRQPAASRDIFAQEPVPPGSGDGLQDALLSLGSDVIDVAGLQQAQVKEALSAPLKVETV	60
Db	1	MRQPAASRDIFAQEPVPPGSGDGLQDALLSLGSDVIDVAGLQQAQVKEALSAPLKVETV	60
Qy	61	YTYLLDGSRLVCEPPELPOEGKVRBAVTSRKRKLCNGLGPSPDLGPKPLARLVAPLAP	120
Db	61	YTYLLDGSRLVCEPPELPOEGKVRBAVTSRKRKLCNGLGPSPDLGPKPLARLVAPLAP	120
Qy	121	DTQVLVPLVDKEGAAVAAILVHCGQLSDNEEWSLQAVEKHTLVALKRVQALQORESSV	180
Db	121	DTQVLVPLVDKEGAAVAAILVHCGQLSDNEEWSLQAVEKHTLVALKRVQALQORESSV	180
Qy	181	APATQNPPEAAGDKGGVAYTNQDKILQICGELYDLDASSILQKLVYLQOQETQASR	240
Db	181	APATQNPPEAAGDKGGVAYTNQDKILQICGELYDLDASSILQKLVYLQOQETQASR	240
Qy	241	CCLLLVSEDNILQLSCKVIGDKVLEEEISFPITTTGRLGQGVVDEKKSILQKDLTSDMQQLQ	300
Db	241	CCLLLVSEDNILQLSCKVIGDKVLEEEISFPITTTGRLGQGVVDEKKSILQKDLTSDMQQLQ	300
Qy	301	SMLGCEVQAMLCVPVISRATDQVVVALACAFNKLGGDLFTDQDEHVIQHCFTYTTVLTST	360
Db	301	SMLGCEVQAMLCVPVISRATDQVVVALACAFNKLGGDLFTDQDEHVIQHCFTYTTVLTST	360
Qy	361	LAFQKEQKLKCEQALLQVAKNLFTHLDDVSVLLQEIITEARNLSNAEICSVFLLDQNEL	420

Db 361 LAFOKEQKLCQKQALLQVAKNLFTHLDDVSVLLQEIITEARNLSNAEICSVFLDQNEL 420  
Qy 421 VAKVFDGGVVEDESEYIRIPADQGIAGHVATTGQILNIPDAYAHPLFYRGVDDSTGFRTR 480  
Db 421 VAKVFDGGVVEDESEYIRIPADQGIAGHVATTGQILNIPDAYAHPLFYRGVDDSTGFRTR 480  
Qy 481 NILCPPIKNEQEVIGVAELVKNKNGPWFSEKDEDLATAFISYCGISIAHSLLYKKVNEA 540  
Db 481 NILCPPIKNEQEVIGVAELVKNKNGPWFSEKDEDLATAFISYCGISIAHSLLYKKVNEA 540  
Qy 541 QYRSHLANEMMYHMKVSDDEYTKLLHDGIPVAAIDSNFASFTYTPRSLPEDDTSMAIL 600  
Db 541 QYRSHLANEMMYHMKVSDDEYTKLLHDGIPVAAIDSNFASFTYTPRSLPEDDTSMAIL 600  
Qy 601 SMLQDMNFINNYKIDCPTLARFCLMVKKGYRDPYPYHNMHAFSVSHFCYLLYKNLELTY 660  
Db 601 SMLQDMNFINNYKIDCPTLARFCLMVKKGYRDPYPYHNMHAFSVSHFCYLLYKNLELTY 660  
Qy 661 LEDMEIFALFISCMCHDLDRGTNNSFOVASKSVLAALYSSEGSVNERHHFAQAIAILNT 720  
Db 661 LEDMEIFALFISCMCHDLDRGTNNSFOVASKSVLAALYSSEGSVNERHHFAQAIAILNT 720  
Qy 721 HGCNIFDHFSRKDYQRMULDMDRDII LATDLAHLRI FKDLQKMAEVGYDRTNKHSLLL 780  
Db 721 HGCNIFDHFSRKDYQRMULDMDRDII LATDLAHLRI FKDLQKMAEVGYDRTNKHSLLL 780  
Qy 781 CLMTSCDLSQDTGKWKTRKIAELIYKEFFSQGDLKAMGNRPMMMDREKAYIPELQI 840  
Db 781 CLMTSCDLSQDTGKWKTRKIAELIYKEFFSQGDLKAMGNRPMMMDREKAYIPELQI 840  
Qy 841 SPMEHAMPIYKLLQDLFPKAAELYERVASNREHMTKVSHTKFTIRGLPSNNSLDFLDBEY 900  
Db 841 SPMEHAMPIYKLLQDLFPKAAELYERVASNREHMTKVSHTKFTIRGLPSNNSLDFLDBEY 900  
Qy 901 EVPDLGAPINGCCSLDAE 921  
Db 901 EVPDLGAPINGCCSLDAE 921

## RESULT 3

US-08-297-510-39  
; Sequence 39, Application US/08297510  
; Patent No. 5602019  
; GENERAL INFORMATION:  
; APPLICANT: Beavo, Joseph A.  
; APPLICANT: Bentley, Kelley  
; APPLICANT: Charbonneau, Harry  
; APPLICANT: Sonnenburg, William K.  
; TITLE OF INVENTION: DNA Encoding Mammalian  
; TITLE OF INVENTION: Phosphodiesterases  
; NUMBER OF SEQUENCES: 58  
; CORRESPONDENCE ADDRESS:  
; ADDRESSEE: Marshall, O'Toole, Gerstein, Murray &  
; ADDRESSEE: Bicknell  
; STREET: Two First National Plaza, 20 South Clark  
; CITY: Chicago  
; STATE: Illinois  
; COUNTRY: USA  
; ZIP: 60603  
; COMPUTER READABLE FORM:  
; MEDIUM TYPE: Floppy disk  
; COMPUTER: IBM PC compatible  
; OPERATING SYSTEM: PC-DOS/MS-DOS  
; SOFTWARE: Patent In Release #1.0, Version #1.25  
; CURRENT APPLICATION DATA:  
; APPLICATION NUMBER: US/08/297,510  
; FILING DATE:  
; CLASSIFICATION: 435  
; PRIOR APPLICATION DATA:  
; APPLICATION NUMBER: US 07/688,356  
; FILING DATE: 04-APR-1991

; ATTORNEY/AGENT INFORMATION:  
; NAME: No. 5602019and, Greta E.  
; REGISTRATION NUMBER: 35,302  
; REFERENCE/DOCKET NUMBER: 27866/30822  
; TELECOMMUNICATION INFORMATION:  
; TELEPHONE: (312) 346-5750  
; TELEFAX: (312) 984-9740  
; TELEX: 25-3856  
; INFORMATION FOR SEQ ID NO: 39:  
; SEQUENCE CHARACTERISTICS:  
; LENGTH: 921 amino acids  
; TYPE: amino acid  
; TOPOLOGY: linear  
; MOLECULE TYPE: protein  
; US-08-297-510-39  
  
Query Match 100.0%; Score 4781; DB 1; Length 921;  
Beat Local Similarity 100.0%; Pred. No. 0;  
Matches 921; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
  
Qy 1 MRRQPAASRDLPFAQEPVPPGSGDQALQDALLSLGSLVIDVAGLQQAQKALSAVLPKQVTV 60  
Db 1 MRRQPAASRDLPFAQEPVPPGSGDQALQDALLSLGSLVIDVAGLQQAQKALSAVLPKQVTV 60  
Qy 61 YTYLLDGSRLVCEPPELPHQEGKQREAVISRKELGCGNLGSPDLPGKPLARLVAPLAP 120  
Db 61 YTYLLDGSRLVCEPPELPHQEGKQREAVISRKELGCGNLGSPDLPGKPLARLVAPLAP 120  
Qy 121 DTQVLVIPLVDEKAGAAVAVILVHCGQLSDNEENSLQAVEKHTLVALKRVQALQOQRESSV 180  
Db 121 DTQVLVIPLVDEKAGAAVAVILVHCGQLSDNEENSLQAVEKHTLVALKRVQALQOQRESSV 180  
Qy 181 APEATQNPPEAAGDQKGVAYTNQDRKILQCGELYDLDASSLQKLVLYLQQTQASR 240  
Db 181 APEATQNPPEAAGDQKGVAYTNQDRKILQCGELYDLDASSLQKLVLYLQQTQASR 240  
Qy 241 CCLLLVSEDNLQLSCKVIGDKVLEESISFPLTTGRLQGVVEDKKISQIKLTSSEDMQQLQ 300  
Db 241 CCLLLVSEDNLQLSCKVIGDKVLEESISFPLTTGRLQGVVEDKKISQIKLTSSEDMQQLQ 300  
Qy 301 SMLGCEVOAMLCVPVISRATQVVALACAFNKLGGDLFTDDEHVIQHFHYTSTVLST 360  
Db 301 SMLGCEVOAMLCVPVISRATQVVALACAFNKLGGDLFTDDEHVIQHFHYTSTVLST 360  
Qy 361 LAFQKEQKLCQKQALLQVAKNLFTHLDDVSVLLQEIITEARNLSNAEICSVFLDQNEL 420  
Db 361 LAFQKEQKLCQKQALLQVAKNLFTHLDDVSVLLQEIITEARNLSNAEICSVFLDQNEL 420  
Qy 421 VAKVFDGGVVEDESEYIRIPADQGIAGHVATTGQILNIPDAYAHPLFYRGVDDSTGFRTR 480  
Db 421 VAKVFDGGVVEDESEYIRIPADQGIAGHVATTGQILNIPDAYAHPLFYRGVDDSTGFRTR 480  
Qy 481 NILCPPIKNEQEVIGVAELVKNKNGPWFSEKDEDLATAFISYCGISIAHSLLYKKVNEA 540  
Db 481 NILCPPIKNEQEVIGVAELVKNKNGPWFSEKDEDLATAFISYCGISIAHSLLYKKVNEA 540  
Qy 541 QYRSHLANEMMYHMKVSDDEYTKLLHDGIPVAAIDSNFASFTYTPRSLPEDDTSMAIL 600  
Db 541 QYRSHLANEMMYHMKVSDDEYTKLLHDGIPVAAIDSNFASFTYTPRSLPEDDTSMAIL 600  
Qy 601 SMLQDMNFINNYKIDCPTLARFCLMVKKGYRDPYPYHNMHAFSVSHFCYLLYKNLELTY 660  
Db 601 SMLQDMNFINNYKIDCPTLARFCLMVKKGYRDPYPYHNMHAFSVSHFCYLLYKNLELTY 660  
Qy 661 LEDMEIFALFISCMCHDLDRGTNNSFOVASKSVLAALYSSEGSVNERHHFAQAIAILNT 720  
Db 661 LEDMEIFALFISCMCHDLDRGTNNSFOVASKSVLAALYSSEGSVNERHHFAQAIAILNT 720  
Qy 721 HGCNIFDHFSRKDYQRMULDMDRDII LATDLAHLRI FKDLQKMAEVGYDRTNKHSLLL 780  
Db 721 HGCNIFDHFSRKDYQRMULDMDRDII LATDLAHLRI FKDLQKMAEVGYDRTNKHSLLL 780  
Qy 781 CLMTSCDLSQDTGKWKTRKIAELIYKEFFSQGDLKAMGNRPMMMDREKAYIPELQI 840

Db 781 CLMTSCDLSQTKGKTRKIAELIYKEFFSQGDLKAMGNRPMMMDREKAYIPELQI 840  
Qy 841 SFMEHIAMPIYKLLQDLFPKAAELYERVASNRHWTQVSHKFTIRGLPSNNSLDFLDBEY 900  
Db 841 SFMEHIAMPIYKLLQDLFPKAAELYERVASNRHWTQVSHKFTIRGLPSNNSLDFLDBEY 900  
Qy 901 EVDPLDGRAPINGCCSLDAE 921  
Db 901 EVDPLDGRAPINGCCSLDAE 921

RESULT 4  
US-08-479-532-39  
; Sequence 39, Application US/08479532  
; Patent No. 5776752  
; GENERAL INFORMATION:  
; APPLICANT: Beavo, Joseph A.  
; APPLICANT: Bentley, Kelley  
; APPLICANT: Charbonneau, Harry  
; APPLICANT: Sonnenburg, William K.  
; TITLE OF INVENTION: DNA Encoding Mammalian  
; TITLE OF INVENTION: Phosphodiesterases  
; NUMBER OF SEQUENCES: 58  
; CORRESPONDENCE ADDRESS:  
; ADDRESSEE: Marshall, O'Toole, Gerstein, Murray &  
; ADDRESSEE: Bicknell  
; STREET: Two First National Plaza, 20 South Clark  
; STREET: Street  
; CITY: Chicago  
; STATE: Illinois  
; COUNTRY: USA  
; ZIP: 60603  
; COMPUTER READABLE FORM:  
; MEDIUM TYPE: Floppy disk  
; COMPUTER: IBM PC compatible  
; OPERATING SYSTEM: PC-DOS/MS-DOS  
; SOFTWARE: PatentIn Release #1.0, Version #1.25  
; CURRENT APPLICATION DATA:  
; APPLICATION NUMBER: US/08/479,532  
; FILING DATE: 07-JUN-1995  
; CLASSIFICATION: 435  
; PRIOR APPLICATION DATA:  
; APPLICATION NUMBER: 08/297,494  
; FILING DATE:  
; APPLICATION NUMBER: US 07/688,356  
; FILING DATE: 04-APR-1991  
; ATTORNEY/AGENT INFORMATION:  
; NAME: No. 5776752and, Greta E.  
; REGISTRATION NUMBER: 35,302  
; REFERENCE/DOCKET NUMBER: 27866/30822  
; TELECOMMUNICATION INFORMATION:  
; TELEPHONE: (312) 346-5750  
; TELEFAX: (312) 984-9740  
; TELEX: 25-3856  
; INFORMATION FOR SEQ ID NO: 39:  
; SEQUENCE CHARACTERISTICS:  
; LENGTH: 921 amino acids  
; TYPE: amino acid  
; TOPOLOGY: linear  
; MOLECULE TYPE: protein  
US-08-479-532-39

Query Match 100.0%; Score 4781; DB 1; Length 921;  
Best Local Similarity 100.0%; Pred. No. 0;  
Matches 921; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 MRQPAASRDLPFAQEPVPPGSGDGLQDALLSLGSLVDVAGLQAVKEALSAVLPKVTY 60  
Db 1 MRQPAASRDLPFAQEPVPPGSGDGLQDALLSLGSLVDVAGLQAVKEALSAVLPKVTY 60  
Qy 61 YTYLLDGSRLVCEPPELHPEQGVREAVISRKRLGCGNGLGPSPDLPGKPLARLVAPLAP 120

Db 61 YTYLLDGSRLVCEPPELHPEQGVREAVISRKRLGCGNGLGPSPDLPGKPLARLVAPLAP 120  
Qy 121 DTQVLVPLVDKEAGAAVILVHCGQLSDNEEWSLOAVERKHTLVALKRVQALQORESSV 180  
Db 121 DTQVLVPLVDKEAGAAVILVHCGQLSDNEEWSLOAVERKHTLVALKRVQALQORESSV 180  
Qy 181 APEATQNPPEAAGDQGGVAYTNNQDRKILQLCCGELYDLDDASSLQQLVQLVQOETOASR 240  
Db 181 APEATQNPPEAAGDQGGVAYTNNQDRKILQLCCGELYDLDDASSLQQLVQLVQOETOASR 240  
Qy 241 CCLLLVSEDNLQLSCKVIGDKVLEEEISFPITTTGRLGQVVEDKKSIQLKDLTSEDMMQQLQ 300  
Db 241 CCLLLVSEDNLQLSCKVIGDKVLEEEISFPITTTGRLGQVVEDKKSIQLKDLTSEDMMQQLQ 300  
Qy 301 SMLGCEVOAMLCPVVISRATDQVVVALACAFNKLGGDLFTDQDEHVIQHCFTYTTSTVLST 360  
Db 301 SMLGCEVOAMLCPVVISRATDQVVVALACAFNKLGGDLFTDQDEHVIQHCFTYTTSTVLST 360  
Qy 361 LAFQEKQLKCECOALLQVAKNLFTHLDDVSVLLQEIITEARNLSNAEICSVFLLDQNEL 420  
Db 361 LAFQEKQLKCECOALLQVAKNLFTHLDDVSVLLQEIITEARNLSNAEICSVFLLDQNEL 420  
Qy 421 VAKVFDGQVVEDESEYIRIPADQGIAGHVATTGQILNIPDAYAHPLFYRGVDDSTGFRTR 480  
Db 421 VAKVFDGQVVEDESEYIRIPADQGIAGHVATTGQILNIPDAYAHPLFYRGVDDSTGFRTR 480  
Qy 481 NILCFPIKNEQEVIGVAELVKNKINGPWFKFDLATAFSIYCGISIAHSLLYKKVNEA 540  
Db 481 NILCFPIKNEQEVIGVAELVKNKINGPWFKFDLATAFSIYCGISIAHSLLYKKVNEA 540  
Qy 541 QYRSHLANEMMMYHMKVSDDEYTKLHDGIQPVAAIDSNFASFTYTPRSLPEDDTSMAIL 600  
Db 541 QYRSHLANEMMMYHMKVSDDEYTKLHDGIQPVAAIDSNFASFTYTPRSLPEDDTSMAIL 600  
Qy 601 SMLQDMNFINNYKIDCPTLARFCLMWKGYRDPYHNMHAFSVSHFCYLLYKNELTNY 660  
Db 601 SMLQDMNFINNYKIDCPTLARFCLMWKGYRDPYHNMHAFSVSHFCYLLYKNELTNY 660  
Qy 661 LEDMEIFALFISCMCHDLHRGTNNSPQVASKSVLAALYSEGSVMRHHFPAQAIANT 720  
Db 661 LEDMEIFALFISCMCHDLHRGTNNSPQVASKSVLAALYSEGSVMRHHFPAQAIANT 720  
Qy 721 HGCNIPDHFSRKDYQRMDLMDRIILATDLAHLURIFKDLQKMAEVGYDRTNKHHSLLL 780  
Db 721 HGCNIPDHFSRKDYQRMDLMDRIILATDLAHLURIFKDLQKMAEVGYDRTNKHHSLLL 780  
Qy 781 CLLMTSCDLSQTKGKTRKIAELIYKEFFSQGDLKAMGNRPMMMDREKAYIPELQI 840  
Db 781 CLLMTSCDLSQTKGKTRKIAELIYKEFFSQGDLKAMGNRPMMMDREKAYIPELQI 840  
Qy 841 SFMEHIAMPIYKLLQDLFPKAAELYERVASNRHWTQVSHKFTIRGLPSNNSLDFLDBEY 900  
Db 841 SFMEHIAMPIYKLLQDLFPKAAELYERVASNRHWTQVSHKFTIRGLPSNNSLDFLDBEY 900  
Qy 901 EVDPLDGRAPINGCCSLDAE 921  
Db 901 EVDPLDGRAPINGCCSLDAE 921

RESULT 5  
US-08-455-526-39  
; Sequence 39, Application US/08455526  
; Patent No. 5789553  
; GENERAL INFORMATION:  
; APPLICANT: Beavo, Joseph A.  
; APPLICANT: Bentley, Kelley  
; APPLICANT: Charbonneau, Harry  
; APPLICANT: Sonnenburg, William K.  
; TITLE OF INVENTION: DNA Encoding Mammalian  
; TITLE OF INVENTION: Phosphodiesterases  
; NUMBER OF SEQUENCES: 58  
; CORRESPONDENCE ADDRESS:  
; ADDRESSEE: Marshall, O'Toole, Gerstein, Murray &







Db 121 DTQVLVPLVDKEAGAAVAVILVHCQQLSDNEEWSLQAVEKHTLVALKRVQALQOQRESSV 180  
Qy 181 APEATONPPEEAGDQKGGVAVTNQDRKILQLCGELYDLDDASSLQQLKVLQYLQOQETQASR 240  
Db 181 APEATONPPEEAGDQKGGVAVTNQDRKILQLCGELYDLDDASSLQQLKVLQYLQOQETQASR 240  
Qy 241 CCLLLVSEDNLQLSCKVIGDKVLEEBISFPPLTTGRLGQVVEDKKSITQLKDLTSEDNQQLQ 300  
Db 241 CCLLLVSEDNLQLSCKVIGDKVLEEBISFPPLTTGRLGQVVEDKKSITQLKDLTSEDNQQLQ 300  
Qy 301 SMLGCEVQAMLCVPVISRATDOVVACAFNKLGGDLFTDQDEHVIQHCFTYSTVLTST 360  
Db 301 SMLGCEVQAMLCVPVISRATDOVVACAFNKLGGDLFTDQDEHVIQHCFTYSTVLTST 360  
Qy 361 LAFQKEQKLKCEQALLQVAKNLFTHLDDVSVLLQEIITEARNLSNAEICSFVLLDQNEL 420  
Db 361 LAFQKEQKLKCEQALLQVAKNLFTHLDDVSVLLQEIITEARNLSNAEICSFVLLDQNEL 420  
Qy 421 VAKVFDGGVVEDESEYIRIPADQGIAGHVATTGQILNIPDAYAHPLFYRGVDDSTGFRTR 480  
Db 421 VAKVFDGGVVEDESEYIRIPADQGIAGHVATTGQILNIPDAYAHPLFYRGVDDSTGFRTR 480  
Qy 481 NILCPPIKNEQVEIGVAELVNKINGPWFSEKFEDELATAFSYCGISIAHSLLYKKVNEA 540  
Db 481 NILCPPIKNEQVEIGVAELVNKINGPWFSEKFEDELATAFSYCGISIAHSLLYKKVNEA 540  
Qy 541 QYRSHLANEMMYHMKVSDDEYTKLLHDGIQPVAIDSNFASFTVTPRSLPDDTSMALL 600  
Db 541 QYRSHLANEMMYHMKVSDDEYTKLLHDGIQPVAIDSNFASFTVTPRSLPDDTSMALL 600  
Qy 601 SMLQDMFNINNYKIDCPTLARFCLMVKKGYRDPYPYHNMHAFSVSHFCYLLYKNLELNY 660  
Db 601 SMLQDMFNINNYKIDCPTLARFCLMVKKGYRDPYPYHNMHAFSVSHFCYLLYKNLELNY 660  
Qy 661 LEDMEIFALFISCMCHDLDRGTNNSFQVASKSVLAALYSSEGSVMERHHFAQAIANT 720  
Db 661 LEDMEIFALFISCMCHDLDRGTNNSFQVASKSVLAALYSSEGSVMERHHFAQAIANT 720  
Qy 721 HGCNIFDHFSRKDYQRMULDLRDII LATDLAHLRI FKDLQKMAEVGYDRTNKQHSLLL 780  
Db 721 HGCNIFDHFSRKDYQRMULDLRDII LATDLAHLRI FKDLQKMAEVGYDRTNKQHSLLL 780  
Qy 781 CLMTSCDLSDOTKGWKTTRKIAELIYKEFPFSGQDLEKAMGNRPMEMMDREKAYIPELQI 840  
Db 781 CLMTSCDLSDOTKGWKTTRKIAELIYKEFPFSGQDLEKAMGNRPMEMMDREKAYIPELQI 840  
Qy 841 SFMEHIAMPIYKLLQDLFPKAAELYERVASNREHWTKVSHKFTIRGLPSNNSLDFLDEY 900  
Db 841 SFMEHIAMPIYKLLQDLFPKAAELYERVASNREHWTKVSHKFTIRGLPSNNSLDFLDEY 900  
Qy 901 EVPLDGDARAPINGCCSLDAE 921  
Db 901 EVPLDGDARAPINGCCSLDAE 921

RESULT 8  
US-09-754-250-5  
; Sequence 5, Application US/09754250  
; Patent No. 6376225  
; GENERAL INFORMATION:  
; APPLICANT: WEI, Ming-Hui et al  
; TITLE OF INVENTION: ISOLATED HUMAN PHOSPHODIESTERASE  
; TITLE OF INVENTION: PROTEINS, NUCLEIC ACID MOLECULES, ENCODING HUMAN  
; TITLE OF INVENTION: PHOSPHODIESTERASE PROTEINS, AND USES THEREOF  
; FILE REFERENCE: CLO01063  
; CURRENT APPLICATION NUMBER: US/09/754,250  
; CURRENT FILING DATE: 2001-01-05  
; NUMBER OF SEQ ID NOS: 5  
; SOFTWARE: FastSeq for Windows Version 4.0  
; SEQ ID NO 5  
; LENGTH: 921  
; TYPE: PRT

; ORGANISM: Bos taurus  
US-09-754-250-5  
Query Match 100.0%; Score 4781; DB 3; Length 921;  
Best Local Similarity 100.0%; Pred. No. 0;  
Matches 921; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
Qy 1 MRQPAASRDLPQAQSPVPPSGDQALQDALLSLGSLVQVAGLQQAQVKEALSAPLKVETV 60  
Db 1 MRQPAASRDLPQAQSPVPPSGDQALQDALLSLGSLVQVAGLQQAQVKEALSAPLKVETV 60  
Qy 61 YTYLLDGSRLVCEPSPHELPOEGKRVREAVISRKLGCGNGLGPSDLPGKPLARLAPLAP 120  
Db 61 YTYLLDGSRLVCEPSPHELPOEGKRVREAVISRKLGCGNGLGPSDLPGKPLARLAPLAP 120  
Qy 121 DTQVLVPLVDKEAGAAVAVILVHCQQLSDNEEWSLQAVEKHTLVALKRVQALQOQRESSV 180  
Db 121 DTQVLVPLVDKEAGAAVAVILVHCQQLSDNEEWSLQAVEKHTLVALKRVQALQOQRESSV 180  
Qy 181 APEATONPPEEAGDQKGGVAVTNQDRKILQLCGELYDLDDASSLQQLKVLQYLQOQETQASR 240  
Db 181 APEATONPPEEAGDQKGGVAVTNQDRKILQLCGELYDLDDASSLQQLKVLQYLQOQETQASR 240  
Qy 241 CCLLLVSEDNLQLSCKVIGDKVLEEBISFPPLTTGRLGQVVEDKKSITQLKDLTSEDNQQLQ 300  
Db 241 CCLLLVSEDNLQLSCKVIGDKVLEEBISFPPLTTGRLGQVVEDKKSITQLKDLTSEDNQQLQ 300  
Qy 301 SMLGCEVQAMLCVPVISRATDOVVACAFNKLGGDLFTDQDEHVIQHCFTYSTVLTST 360  
Db 301 SMLGCEVQAMLCVPVISRATDOVVACAFNKLGGDLFTDQDEHVIQHCFTYSTVLTST 360  
Qy 361 LAFQKEQKLKCEQALLQVAKNLFTHLDDVSVLLQEIITEARNLSNAEICSFVLLDQNEL 420  
Db 361 LAFQKEQKLKCEQALLQVAKNLFTHLDDVSVLLQEIITEARNLSNAEICSFVLLDQNEL 420  
Qy 421 VAKVFDGGVVEDESEYIRIPADQGIAGHVATTGQILNIPDAYAHPLFYRGVDDSTGFRTR 480  
Db 421 VAKVFDGGVVEDESEYIRIPADQGIAGHVATTGQILNIPDAYAHPLFYRGVDDSTGFRTR 480  
Qy 481 NILCPPIKNEQVEIGVAELVNKINGPWFSEKFEDELATAFSYCGISIAHSLLYKKVNEA 540  
Db 481 NILCPPIKNEQVEIGVAELVNKINGPWFSEKFEDELATAFSYCGISIAHSLLYKKVNEA 540  
Qy 541 QYRSHLANEMMYHMKVSDDEYTKLLHDGIQPVAIDSNFASFTVTPRSLPDDTSMALL 600  
Db 541 QYRSHLANEMMYHMKVSDDEYTKLLHDGIQPVAIDSNFASFTVTPRSLPDDTSMALL 600  
Qy 601 SMLQDMFNINNYKIDCPTLARFCLMVKKGYRDPYPYHNMHAFSVSHFCYLLYKNLELNY 660  
Db 601 SMLQDMFNINNYKIDCPTLARFCLMVKKGYRDPYPYHNMHAFSVSHFCYLLYKNLELNY 660  
Qy 661 LEDMEIFALFISCMCHDLDRGTNNSFQVASKSVLAALYSSEGSVMERHHFAQAIANT 720  
Db 661 LEDMEIFALFISCMCHDLDRGTNNSFQVASKSVLAALYSSEGSVMERHHFAQAIANT 720  
Qy 721 HGCNIFDHFSRKDYQRMULDLRDII LATDLAHLRI FKDLQKMAEVGYDRTNKQHSLLL 780  
Db 721 HGCNIFDHFSRKDYQRMULDLRDII LATDLAHLRI FKDLQKMAEVGYDRTNKQHSLLL 780  
Qy 781 CLMTSCDLSDOTKGWKTTRKIAELIYKEFPFSGQDLEKAMGNRPMEMMDREKAYIPELQI 840  
Db 781 CLMTSCDLSDOTKGWKTTRKIAELIYKEFPFSGQDLEKAMGNRPMEMMDREKAYIPELQI 840  
Qy 841 SFMEHIAMPIYKLLQDLFPKAAELYERVASNREHWTKVSHKFTIRGLPSNNSLDFLDEY 900  
Db 841 SFMEHIAMPIYKLLQDLFPKAAELYERVASNREHWTKVSHKFTIRGLPSNNSLDFLDEY 900  
Qy 901 EVPLDGDARAPINGCCSLDAE 921  
Db 901 EVPLDGDARAPINGCCSLDAE 921

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US-09-883-825-39
; Sequence 39, Application US/09883825
; Patent No. 6842040
; GENERAL INFORMATION:
; APPLICANT: Beavo, Joseph A.
; Bentley, Kelley
; Charbonneau, Harry
; Sonnenburg, William K.
; TITLE OF INVENTION: DNA Encoding Mammalian
; Phosphodiesterases
; NUMBER OF SEQUENCES: 58
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Marshall, O'Toole, Gerstein, Murray &
; Bicknell
; STREET: Two First National Plaza, 20 South Clark
; Street
; CITY: Chicago
; STATE: Illinois
; COUNTRY: USA
; ZIP: 60603
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patent In Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/883,825
; FILING DATE: 18-Jun-2001
; CLASSIFICATION: <Unknown>
; PRIORITY APPLICATION DATA:
; APPLICATION NUMBER: 09/123,783
; FILING DATE: <Unknown>
; APPLICATION NUMBER: 08/297,494
; FILING DATE: <Unknown>
; APPLICATION NUMBER: US 07/688,356
; FILING DATE: 04-APR-1991
; ATTORNEY/AGENT INFORMATION:
; NAME: No. 6642040and, Greta E.
; REGISTRATION NUMBER: 35,302
; REFERENCE/DOCKET NUMBER: 27866/30822
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (312) 346-5750
; TELEFAX: (312) 984-9740
; TELEX: 25-3856
; INFORMATION FOR SEQ ID NO: 39:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 921 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: protein
; SEQUENCE DESCRIPTION: SEQ ID NO: 39:
US-09-883-825-39
Query Match 100.0%; Score 4781; DB 4; Length 921;
Best Local Similarity 100.0%; Pred. No. 0;
Matches 921; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
Qy 1 MRRQPAASRDLPFAQEPVPPGSGDGLQDALLSLGSLVDVAGLQQAQVKEALSAPLKVETV 60
Db 1 MRRQPAASRDLPFAQEPVPPGSGDGLQDALLSLGSLVDVAGLQQAQVKEALSAPLKVETV 60
Qy 61 YTYLLDGSRLVCEPPELPHQEGKVRBAVSRKRLGCGNGLGPSSDLPGKPLARLVAPLAP 120
Db 61 YTYLLDGSRLVCEPPELPHQEGKVRBAVSRKRLGCGNGLGPSSDLPGKPLARLVAPLAP 120
Qy 121 DTQVLVPLVDKEAGAAVAVILVHCGQLSDNEEWSLQAVEKHTLVALKRVQALQORESSV 180
Db 121 DTQVLVPLVDKEAGAAVAVILVHCGQLSDNEEWSLQAVEKHTLVALKRVQALQORESSV 180
Qy 181 APEATQNPPEAAGDQKGQVATYQDRKILQCGELYDLDASSLQLKVLQYLOQETQASR 240
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Qy 241 CCLLLVSEDNLQLSCKVIGDKVLEEEISFPLTTGRLGOVVEDKKSIOQLKDLTSEDMOQLQ 300
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Qy 301 SMLGCEVQAMLCVPIISRATDQVVALACAFNKLGGDLFTDQDEHVIQHCFTYTSVLTST 360
Db 301 SMLGCEVQAMLCVPIISRATDQVVALACAFNKLGGDLFTDQDEHVIQHCFTYTSVLTST 360
Qy 361 LAFQEKQKLCCEQALLQVAKNLFTHLDDVSVLQEIITEARNLSNAEICSVFLLDQNEL 420
Db 361 LAFQEKQKLCCEQALLQVAKNLFTHLDDVSVLQEIITEARNLSNAEICSVFLLDQNEL 420
Qy 421 VAKVFDGGVDESEYIRIPADQGIAGHVATTGQLNIPDAYAHPLEFVRGVDDSGFRTR 480
Db 421 VAKVFDGGVDESEYIRIPADQGIAGHVATTGQLNIPDAYAHPLEFVRGVDDSGFRTR 480
Qy 481 NILCFPIKNENQEVIGVAELVNKINGPWFSKFDEDLATAFSIYCGISIAHSLLYKKVNEA 540
Db 481 NILCFPIKNENQEVIGVAELVNKINGPWFSKFDEDLATAFSIYCGISIAHSLLYKKVNEA 540
Qy 541 QYRSHLANEMMMYHMKVSDDEYTKLHDGIQPVAAIDSNFASFTYTPRSLPEDDTSMAIL 600
Db 541 QYRSHLANEMMMYHMKVSDDEYTKLHDGIQPVAAIDSNFASFTYTPRSLPEDDTSMAIL 600
Qy 601 SMLQDMNFINNYKIDCPTLARFCLMVKKGYRDPYHNMHAFSVSHFCYLLYKNLELTNY 660
Db 601 SMLQDMNFINNYKIDCPTLARFCLMVKKGYRDPYHNMHAFSVSHFCYLLYKNLELTNY 660
Qy 661 LEDMEIFALFTSCMCHDLHRGTNNNSFQVASKSVLAALYSSEGSVMERHHPAQAIILNT 720
Db 661 LEDMEIFALFTSCMCHDLHRGTNNNSFQVASKSVLAALYSSEGSVMERHHPAQAIILNT 720
Qy 721 HGCNIFDHFSRKQYQRMILMDRIILATDLAHLRIKFDLQKMAEVGYDRTNKQHHSLLL 780
Db 721 HGCNIFDHFSRKQYQRMILMDRIILATDLAHLRIKFDLQKMAEVGYDRTNKQHHSLLL 780
Qy 781 CLLMTSCDLSDOTGKWKTKRIAEIYKEPFSQGDLEKAMGNRPMEMMDREKAYIPELQI 840
Db 781 CLLMTSCDLSDOTGKWKTKRIAEIYKEPFSQGDLEKAMGNRPMEMMDREKAYIPELQI 840
Qy 841 SFMEHIAMPYIKLIQDLFPKAAELYERVAENREHWTKVSHKFTIRGLPSNNSLDFLDEEY 900
Db 841 SFMEHIAMPYIKLIQDLFPKAAELYERVAENREHWTKVSHKFTIRGLPSNNSLDFLDEEY 900
Qy 901 EVDPLDGAAPINGCCSLDAE 921
Db 901 EVDPLDGAAPINGCCSLDAE 921
RESULT 10
PCT-US92-03222-39
; Sequence 39, Application PC/TUS9203222
; GENERAL INFORMATION:
; APPLICANT: Beavo, Joseph A.
; APPLICANT: Bentley, Kelley
; APPLICANT: Charbonneau, Harry
; APPLICANT: Sonnenburg, William K.
; TITLE OF INVENTION: DNA Encoding Mammalian
; Phosphodiesterases
; NUMBER OF SEQUENCES: 58
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Marshall, O'Toole, Gerstein, Murray &
; Bicknell
; STREET: Two First National Plaza, 20 South Clark
; CITY: Chicago
; STATE: Illinois
; COUNTRY: USA
; ZIP: 60603
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
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SOFTWARE: PatentIn Release #1.0, Version #1.25  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: PCT/US92/03222  
FILING DATE: 19920420  
CLASSIFICATION: 435  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: US 07/688,356  
FILING DATE: 04-APR-1991  
ATTORNEY/AGENT INFORMATION:  
NAME: Noland, Greta E.  
REGISTRATION NUMBER: 35,302  
REFERENCE/DOCKET NUMBER: 27866/30822  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: (312) 346-5750  
TELEFAX: (312) 984-9740  
TELEX: 25-3856  
INFORMATION FOR SEQ ID NO: 39:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 921 amino acids  
TYPE: AMINO ACID  
TOPOLOGY: linear  
MOLECULE TYPE: protein  
PCT-US92-03222-39

Query Match 100.0%; Score 4781; DB 5; Length 921;  
Best Local Similarity 100.0%; Pred. No. 0;  
Matches 921; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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DB 1 MRQPAAARDLPAQEPVPPGSGDGLQDALLSLGSDVIVAGLQQAQKALSAVLPKVTY 60

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DB 61 YTYLLDGSRLCEPPEHPHLPQEGKRVREAVISRKRLGCGNGLGPSDLPGKPLARLVAPLAP 120

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DB 121 DTQVLVPLVDKEAGAAVAILVHCGQLSDNEBSLQAVEKHTLVALKRVQALQORESSV 180

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DB 181 APEATONPPEAAGOKGGVATNDRKTLQCGELYDLDASSLQQLKVLQYLOQTQASR 240

QY 241 CCLLLVSDNLQLSCKVIGDKVLESEISFPLTTGRLGQVVEDKSIQKDLTSEDMMQQLQ 300  
DB 241 CCLLLVSDNLQLSCKVIGDKVLESEISFPLTTGRLGQVVEDKSIQKDLTSEDMMQQLQ 300

QY 301 SMLGCEVQAMLCVPVISRATDQVVALACAFNKLGGDLFTDQDEHVIQHCFTYSTVLST 360  
DB 301 SMLGCEVQAMLCVPVISRATDQVVALACAFNKLGGDLFTDQDEHVIQHCFTYSTVLST 360

QY 361 LAFQKEQKLKCEQALLQVAKNLFTHLDDVSVLQELIITEARNLSNAEICSVFLLDQNEL 420  
DB 361 LAFQKEQKLKCEQALLQVAKNLFTHLDDVSVLQELIITEARNLSNAEICSVFLLDQNEL 420

QY 421 VAKVFDGCVGVESEYIIRIPADQGIAGHVATTGQILNIPDAYHPLFYRGVDDSGFRT 480  
DB 421 VAKVFDGCVGVESEYIIRIPADQGIAGHVATTGQILNIPDAYHPLFYRGVDDSGFRT 480

QY 481 NILCFPIKNQEVIGVAELVNKINGPWFSPFDEDLATAFSIYCGISIAHSLLYKKVNEA 540  
DB 481 NILCFPIKNQEVIGVAELVNKINGPWFSPFDEDLATAFSIYCGISIAHSLLYKKVNEA 540

QY 541 QYRSHLANEMMYHMKVSDDEYTKLLHDGIQPVAAIDSNFASFTYTPSLPEDDTSMAIL 600  
DB 541 QYRSHLANEMMYHMKVSDDEYTKLLHDGIQPVAAIDSNFASFTYTPSLPEDDTSMAIL 600

QY 601 SMLQDMFINNYKIDCPTLARFCLMVKKGYRDPYPVHNMWHPFSVSHFCVLLYKNLELNY 660  
DB 601 SMLQDMFINNYKIDCPTLARFCLMVKKGYRDPYPVHNMWHPFSVSHFCVLLYKNLELNY 660

QY 661 LEDMEIFALFISCMCHDLHRGTNNNSFQVASKSVLAALYSSEGSMYRHHFAQAIILNT 720

DB 661 LEDMEIFALFISCMCHDLHRGTNNNSFQVASKSVLAALYSSEGSMYRHHFAQAIILNT 720  
QY 721 HGCNIFDHFSDYQYQMLDLMRDIIILATDLAHLRIFFKDLQKMAEYGYDRTNKHHSLLL 780  
DB 721 HGCNIFDHFSDYQYQMLDLMRDIIILATDLAHLRIFFKDLQKMAEYGYDRTNKHHSLLL 780

QY 781 CLLTMSCDLSQDTKGWKTTRKIAELIYKFFSQGDLKAMGNRPMEMMDREKAYIPELQI 840  
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QY 841 SPMEHIAMPIYKLLQDLFPKAAELYERVASNEHHTKVSHKETIRGLPSNNSLDFLDEY 900  
DB 841 SPMEHIAMPIYKLLQDLFPKAAELYERVASNEHHTKVSHKETIRGLPSNNSLDFLDEY 900

QY 901 EVPDLGAGARAPINGCCSLDAE 921  
DB 901 EVPDLGAGARAPINGCCSLDAE 921

RESULT 11  
US-07-872-644-43  
Sequence 43, Application US/07872644  
Patent No. 5389527  
GENERAL INFORMATION:  
APPLICANT: Beavo, Joseph A.  
APPLICANT: Bentley, Kelley  
APPLICANT: Charbonneau, Harry  
APPLICANT: Sonnenburg, William K.  
TITLE OF INVENTION: DNA Encoding Mammalian  
TITLE OF INVENTION: Phosphodiesterases  
NUMBER OF SEQUENCES: 58  
CORRESPONDENCE ADDRESS:  
ADDRESS: Marshall, O'Toole, Gerstein, Murray &  
ADDRESS: Bicknell,  
STREET: Two First National Plaza, 20 South Clark  
CITY: Chicago  
STATE: Illinois  
COUNTRY: USA  
ZIP: 60603  
COMPUTER READABLE FORM:  
MEDIUM TYPE: Floppy disk  
COMPUTER: IBM PC compatible  
OPERATING SYSTEM: PC-DOS/MS-DOS  
SOFTWARE: PatentIn Release #1.0, Version #1.25  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/07/872,644  
FILING DATE: 19920420  
CLASSIFICATION: 435  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: US 07/688,356  
FILING DATE: 04-APR-1991  
ATTORNEY/AGENT INFORMATION:  
NAME: No. 5389527and, Greta E.  
REGISTRATION NUMBER: 35,302  
REFERENCE/DOCKET NUMBER: 27866/30822  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: (312) 346-5750  
TELEFAX: (312) 984-9740  
TELEX: 25-3856  
INFORMATION FOR SEQ ID NO: 43:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 942 amino acids  
TYPE: AMINO ACID  
TOPOLOGY: linear  
MOLECULE TYPE: protein  
US-07-872-644-43

Query Match 97.4%; Score 4657; DB 1; Length 942;  
Best Local Similarity 98.9%; Pred. No. 0;  
Matches 898; Conservative 3; Mismatches 7; Indels 0; Gaps 0;



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QY 434 SYEIRIPADOGIAGHVATTGQIILNIPDAYAHPLPYRGVDDSTGFRTRNLTCLPFKNQOE 493
Db 455 SYEIRIPADOGIAGHVATTGQIILNIPDAYAHPLPYRGVDDSTGFRTRNLTCLPFKNQOE 514
QY 494 VIGVAELVNKINGPWFESKPEDLATAFSIYCGISIAHSLLYKKVNEAQYRSHLANEMMY 553
Db 515 VIGVAELVNKINGPWFESKPEDLATAFSIYCGISIAHSLLYKKVNEAQYRSHLANEMMY 574
QY 554 HMKVSDDEYTKLLHDGIQPVAAIDSNFASFTYTPRSLPEDDTSMALLSMLQDMNFNNYK 613
Db 575 HMKVSDDEYTKLLHDGIQPVAAIDSNFASFTYTPRSLPEDDTSMALLSMLQDMNFNNYK 634
QY 614 IDCPTLARFCMLVKKGYRDPYVHNMHAFSVSHFCYLLLYKNELTNYLDEMEIFALFISC 673
Db 635 IDCPTLARFCMLVKKGYRDPYVHNMHAFSVSHFCYLLLYKNELTNYLDEMEIFALFISC 694
QY 674 MCHDLDRGTNNNSFQVASKSVLAALYSSEGSVMERHHFAQAIAILNTHGNCNIFDHF SRKD 733
Db 695 MCHDLDRGTNNNSFQVASKSVLAALYSSEGSVMERHHFAQAIAILNTHGNCNIFDHF SRKD 754
QY 734 YQRMOLDLMDRIILATDLAHLRIFFKDLQKMAEYGVYDRTNKHSHSLLLCLLMTSCDLS DQT 793
Db 755 YQRMOLDLMDRIILATDLAHLRIFFKDLQKMAEYGVYDRTNKHSHSLLLCLLMTSCDLS DQT 814
QY 794 KGWKTTRKIAELIYKEFFSQGDLEKAMGNRPMEHMDREKAYIPELOISFMEHIAMPIYKL 853
Db 815 KGWKTTRKIAELIYKEFFSQGDLEKAMGNRPMEHMDREKAYIPELOISFMEHIAMPIYKL 874
QY 854 LODLPFAELYERVAASREHMTKVSHKFTIRGLPSNNSLDFLDEVEYVDPDLDGARAPIN 913
Db 875 LODLPFAELYERVAASREHMTKVSHKFTIRGLPSNNSLDFLDEVEYVDPDLDGARAPIN 934
QY 914 GCCLSDAE 921
Db 935 GCCLSDAE 942

RESULT 13
US-08-297-510-43
; Sequence 43, Application US/08297510
; Patent No. 5602019
; GENERAL INFORMATION:
; APPLICANT: Beavo, Joseph A.
; APPLICANT: Bentley, Kelley
; APPLICANT: Charbonneau, Harry
; APPLICANT: Sonnenburg, William K.
; TITLE OF INVENTION: DNA Encoding Mammalian
; TITLE OF INVENTION: Phosphodiesterases
; NUMBER OF SEQUENCES: 58
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Marshall, O'Toole, Gerstein, Murray &
; ADDRESSEE: Bicknell
; STREET: Two First National Plaza, 20 South Clark
; STREET: Street
; CITY: Chicago
; STATE: Illinois
; COUNTRY: USA
; ZIP: 60603
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patent In Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/297,510
; FILING DATE:
; CLASSIFICATION: 435
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 07/688,356
; FILING DATE: 04-APR-1991
; ATTORNEY/AGENT INFORMATION:
; NAME: No. 5602019and, Greta E.
; REGISTRATION NUMBER: 35,302
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; REFERENCE/DOCKET NUMBER: 27866/30822
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (312) 346-5750
; TELEFAX: (312) 984-9740
; TELEX: 25-3856
; INFORMATION FOR SEQ ID NO: 43:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 942 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: protein
; US-08-297-510-43

Query Match 97.4%; Score 4657; DB 1; Length 942;
Best Local Similarity 98.9%; Pred. No. 0;
Matches 898; Conservative 3; Mismatches 7; Indels 0; Gaps 0;

QY 14 QBPVPGSGDGLQDALLSLGSDVIDVAGLQQAQKALSAVLPKVETVYTYLLDGSRLVC 73
Db 35 EBPFPQPQCADSLQDALLSLGSDVIDVAGLQQAQKALSAVLPKVETVYTYLLDGSRLVC 94
QY 74 EBPFPHELPOEGKVRNAVISRKELGNGLGPSDLPGKPLARLVAPLAPDTQVLVPLVDXE 133
Db 95 EBPFPHELPOEGKVRNAVISRKELGNGLGPSDLPGKPLARLVAPLAPDTQVLVPLVDXE 154
QY 134 AGAAVAATLVHCGQLSDNEEWSLQAVEKHTLVALKRVQALQORESSVAPEATQNPPEEA 193
Db 155 AGAAVAATLVHCGQLSDNEEWSLQAVEKHTLVALKRVQALQORESSVAPEATQNPPEEA 214
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Db 215 GQKGGVATYTDQDKILQCGELYDLDAASSLQKVLQYLLQQTQASRCCLLLVSEDLQL 274
QY 254 SCKVIGDKVLEEEISFPPLTTGRIGQVVEDKGIQKDLTSEDMMQQLQSMGLGEVQAMLCV 313
Db 275 SCKVIGDKVLEEEISFPPLTTGRIGQVVEDKGIQKDLTSEDMMQQLQSMGLGEVQAMLCV 334
QY 314 PVISRATDQVVALACAFNKLGGDLFTDQDEHVIQHCFTYTVLTSTLAFQKEQKLKCEC 373
Db 335 PVISRATDQVVALACAFNKLGGDLFTDQDEHVIQHCFTYTVLTSTLAFQKEQKLKCEC 394
QY 374 QALLQVAKNLFTHLDDVSVLLQEIITEARNLSNABEICSVFLDDQNELVAKVDFGGVVEDE 433
Db 395 QALLQVAKNLFTHLDDVSVLLQEIITEARNLSNABEICSVFLDDQNELVAKVDFGGVVEDE 454
QY 434 SYEIRIPADOGIAGHVATTGQIILNIPDAYAHPLPYRGVDDSTGFRTRNLTCLPFKNQOE 493
Db 455 SYEIRIPADOGIAGHVATTGQIILNIPDAYAHPLPYRGVDDSTGFRTRNLTCLPFKNQOE 514
QY 494 VIGVAELVNKINGPWFESKPEDLATAFSIYCGISIAHSLLYKKVNEAQYRSHLANEMMY 553
Db 515 VIGVAELVNKINGPWFESKPEDLATAFSIYCGISIAHSLLYKKVNEAQYRSHLANEMMY 574
QY 554 HMKVSDDEYTKLLHDGIQPVAAIDSNFASFTYTPRSLPEDDTSMALLSMLQDMNFNNYK 613
Db 575 HMKVSDDEYTKLLHDGIQPVAAIDSNFASFTYTPRSLPEDDTSMALLSMLQDMNFNNYK 634
QY 614 IDCPTLARFCMLVKKGYRDPYVHNMHAFSVSHFCYLLLYKNELTNYLDEMEIFALFISC 673
Db 635 IDCPTLARFCMLVKKGYRDPYVHNMHAFSVSHFCYLLLYKNELTNYLDEMEIFALFISC 694
QY 674 MCHDLDRGTNNNSFQVASKSVLAALYSSEGSVMERHHFAQAIAILNTHGNCNIFDHF SRKD 733
Db 695 MCHDLDRGTNNNSFQVASKSVLAALYSSEGSVMERHHFAQAIAILNTHGNCNIFDHF SRKD 754
QY 734 YQRMOLDLMDRIILATDLAHLRIFFKDLQKMAEYGVYDRTNKHSHSLLLCLLMTSCDLS DQT 793
Db 755 YQRMOLDLMDRIILATDLAHLRIFFKDLQKMAEYGVYDRTNKHSHSLLLCLLMTSCDLS DQT 814
QY 794 KGWKTTRKIAELIYKEFFSQGDLEKAMGNRPMEHMDREKAYIPELOISFMEHIAMPIYKL 853
Db 815 KGWKTTRKIAELIYKEFFSQGDLEKAMGNRPMEHMDREKAYIPELOISFMEHIAMPIYKL 874
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QY 854 LQDLFPKAAELYERVASNRHWTQVSHKFTIRGLPSNNSLDFLDEEYEVDPDLDGARAPIN 913  
Db 875 LQDLFPKAAELYERVASNRHWTQVSHKFTIRGLPSNNSLDFLDEEYEVDPDLDGARAPIN 934  
QY 914 GCCSLDAE 921  
Db 935 GCCSLDAE 942

RESULT 14  
US-08-479-532-43  
; Sequence 43, Application US/08479532  
; Patent No. 5776752  
; GENERAL INFORMATION:  
; APPLICANT: Beavo, Joseph A.  
; APPLICANT: Bentley, Kelley  
; APPLICANT: Charbonneau, Harry  
; APPLICANT: Sonnenburg, William K.  
; TITLE OF INVENTION: DNA Encoding Mammalian  
; TITLE OF INVENTION: Phosphodiesterases  
; NUMBER OF SEQUENCES: 58  
; CORRESPONDENCE ADDRESS:  
; ADDRESSEE: Marshall, O'Toole, Gerstein, Murray &  
; ADDRESSEE: Bicknell  
; STREET: Two First National Plaza, 20 South Clark  
; STREET: Street  
; CITY: Chicago  
; STATE: Illinois  
; COUNTRY: USA  
; ZIP: 60603  
; COMPUTER READABLE FORM:  
; MEDIUM TYPE: Floppy disk  
; COMPUTER: IBM PC compatible  
; OPERATING SYSTEM: PC-DOS/MS-DOS  
; SOFTWARE: PatentIn Release #1.0, Version #1.25  
; CURRENT APPLICATION DATA:  
; APPLICATION NUMBER: US/08/479,532  
; FILING DATE: 07-JUN-1995  
; CLASSIFICATION: 435  
; PRIOR APPLICATION DATA:  
; APPLICATION NUMBER: 08/297,494  
; FILING DATE:  
; APPLICATION NUMBER: US 07/688,356  
; FILING DATE: 04-APR-1991  
; ATTORNEY/AGENT INFORMATION:  
; NAME: No. 5776752and, Greta E.  
; REGISTRATION NUMBER: 35,302  
; REFERENCE/DOCKET NUMBER: 27866/30822  
; TELECOMMUNICATION INFORMATION:  
; TELEPHONE: (312) 346-5750  
; TELEFAX: (312) 984-9740  
; TELEX: 25-3856  
; INFORMATION FOR SEQ ID NO: 43:  
; SEQUENCE CHARACTERISTICS:  
; LENGTH: 942 amino acids  
; TYPE: amino acid  
; TOPOLOGY: linear  
; MOLECULE TYPE: protein  
US-08-479-532-43

Query Match 97.4%; Score 4657; DB 1; Length 942;  
Best Local Similarity 98.9%; Pred. No. 0;  
Matches 898; Conservative 3; Mismatches 7; Indels 0; Gaps 0;

QY 14 QEPVPPGSGDQALQDALLSLGSDIVDAGLQQAQVKEALSAPVLPKVTYVTVYLLDGSRLVC 73  
Db 35 EPPPPQPCADSLQDALLSLGSDIVDAGLQQAQVKEALSAPVLPKVTYVTVYLLDGSRLVC 94  
QY 74 BEPPHELPOEGKVRKRAVTSRRLGNCGLGSPDLPKPLARLVAPLADPTQVLVPLVDKE 133  
Db 95 BEPPHELPOEGKVRKRAVTSRRLGNCGLGSPDLPKPLARLVAPLADPTQVLVPLVDKE 154  
QY 134 AGAVALVILVHCGQLSDNEWSLQAVEKHTLVALKRVQALQORESSVAPATQNPPEAA 193

Db 155 AGAVALVILVHCGQLSDNEWSLQAVEKHTLVALKRVQALQORESSVAPATQNPPEAA 214  
QY 194 GDQKGGVAYTNQDRKILQLCGELYDLDAASSLQKLVLYLQOETQASRCLLLVSDNLQL 253  
Db 215 GDQKGGVAYTDQDRKILQLCGELYDLDAASSLQKLVLYLQOETQASRCLLLVSDNLQL 274  
QY 254 SKVIGDKVLLEEISFPPLTTGRLGQVVEDKKSIOIKDLTSEDMOQLQSMGCEVQAMLCV 313  
Db 275 SKVIGDKVLLEEISFPPLTTGRLGQVVEDKKSIOIKDLTSEDMOQLQSMGCEVQAMLCV 334  
QY 314 PVISRATDQVVALACAFNKLGGDLFTQDDEHVIQHCFTYTSVLTSTLAFQKQKLCCEC 373  
Db 335 PVISRATDQVVALACAFNKLGGDLFTQDDEHVIQHCFTYTSVLTSTLAFQKQKLCCEC 394  
QY 374 QALLQVAKNLFTHLDDVSVLLQEIITEARNLSNAEISCVFLLDQNELVAKVFDGGVDE 433  
Db 395 QALLQVAKNLFTHLDDVSVLLQEIITEARNLSNAEISCVFLLDQNELVAKVFDGGVDE 454  
QY 434 SYEIRIPADQGIAGHVATTGOILNIPDAYAHLFVYRGVDDSTGFRTRNLCFPIKNEOE 493  
Db 455 SYEIRIPADQGIAGHVATTGOILNIPDAYAHLFVYRGVDDSTGFRTRNLCFPIKNEOE 514  
QY 494 VIGVAELVNKINGPWFKFDLATAFSIYCGISIAHSLLYKKNVNAQYRSHLANEMMY 553  
Db 515 VIGVAELVNKINGPWFKFDLATAFSIYCGISIAHSLLYKKNVNAQYRSHLANEMMY 574  
QY 554 HMKVSDDEYTKLLHDGIQPVAAIDSNFASFTYTPRSIPEDDTSMALLSMLQDMFNNYK 613  
Db 575 HMKVSDDEYTKLLHDGIQPVAAIDSNFASFTYTPRSIPEDDTSMALLSMLQDMFNNYK 634  
QY 614 IDCPTLARFCLMVKKGYRDPYHNWMAFVSHECYLLYKNLELTNYLEDMEIFALFTSC 673  
Db 635 IDCPTLARFCLMVKKGYRDPYHNWMAFVSHECYLLYKNLELTNYLEDMEIFALFTSC 694  
QY 674 MCHDLDRGTNNSPQVASKSVLAALYSSEGSMRHHFAQAIATLTHGNCIFDHFSRKD 733  
Db 695 MCHDLDRGTNNSPQVASKSVLAALYSSEGSMRHHFAQAIATLTHGNCIFDHFSRKD 754  
QY 734 YQRLDLMRDIILATDLAHLRIFKDLQKMAEVGYDRTNKHHSLLCLLMTSCDLSQOT 793  
Db 755 YQRLDLMRDIILATDLAHLRIFKDLQKMAEVGYDRTNKHHSLLCLLMTSCDLSQOT 814  
QY 794 KGWKTTRKIAELIYKEFFSQGDLKAMGNRPMWMDREKAYIPELQISFMHIAPIYKL 853  
Db 815 KGWKTTRKIAELIYKEFFSQGDLKAMGNRPMWMDREKAYIPELQISFMHIAPIYKL 874  
QY 854 LQDLFPKAAELYERVASNRHWTQVSHKFTIRGLPSNNSLDFLDEEYEVDPDLDGARAPIN 913  
Db 875 LQDLFPKAAELYERVASNRHWTQVSHKFTIRGLPSNNSLDFLDEEYEVDPDLDGARAPIN 934  
QY 914 GCCSLDAE 921  
Db 935 GCCSLDAE 942

RESULT 15  
US-08-455-526-43  
; Sequence 43, Application US/08455526  
; Patent No. 5789553  
; GENERAL INFORMATION:  
; APPLICANT: Beavo, Joseph A.  
; APPLICANT: Bentley, Kelley  
; APPLICANT: Charbonneau, Harry  
; APPLICANT: Sonnenburg, William K.  
; TITLE OF INVENTION: DNA Encoding Mammalian  
; TITLE OF INVENTION: Phosphodiesterases  
; NUMBER OF SEQUENCES: 58  
; CORRESPONDENCE ADDRESS:  
; ADDRESSEE: Marshall, O'Toole, Gerstein, Murray &  
; ADDRESSEE: Bicknell  
; STREET: Two First National Plaza, 20 South Clark  
; STREET: Street



CITY: Chicago  
STATE: Illinois  
COUNTRY: USA  
ZIP: 60603  
COMPUTER READABLE FORM:  
MEDIUM TYPE: Floppy disk  
COMPUTER: IBM PC compatible  
OPERATING SYSTEM: PC-DOS/MS-DOS  
SOFTWARE: Patent In Release #1.0, Version #1.25  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/08/455,526  
FILING DATE: 31-MAY-1995  
CLASSIFICATION: 530  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: US 08/297,494  
FILING DATE: 29-AUG-1994  
APPLICATION NUMBER: US 07/688,356  
FILING DATE: 04-APR-1991  
ATTORNEY/AGENT INFORMATION:  
NAME: NO. 5789553and, Greta E.  
REGISTRATION NUMBER: 35,302  
REFERENCE/DOCKET NUMBER: 27866/30822  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: (312) 346-5750  
TELEFAX: (312) 984-9740  
TELEX: 25-3856  
INFORMATION FOR SEQ ID NO: 43:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 942 amino acids  
TYPE: amino acid  
TOPOLOGY: linear  
MOLECULE TYPE: protein  
US-08-455-526-43

Query Match 97.4%; Score 4657; DB 1; Length 942;  
Best Local Similarity 98.9%; Pred. No. 0;  
Matches 898; Conservative 3; Mismatches 7; Indels 0; Gaps 0;

Qy	14	QBPPVPGSGDQALDALLSLGSDVIDVAGLQQAQVEALS	AVLPKVTETVTVYLLDGSRLVC	73
Db	35	EBPPPPQPCADSLQDALLSLGSDVIDVAGLQQAQVEALS	AVLPKVTETVTVYLLDGSRLVC	94
Qy	74	EBPPHELPOEGKVRBAVSRKRLGNGLGPSDLPGKPLARL	VAPLAPDTQVLVIPLVDKE	133
Db	95	EBPPHELPOEGKVRBAVSRKRLGNGLGPSDLPGKPLARL	VAPLAPDTQVLVIPLVDKE	154
Qy	134	AGAAVAATLVHCGQLSDNEEWSLQAVEKHTLVALKRVQ	ALQOQRESSVAPETONPPEAA	193
Db	155	AGAAVAATLVHCGQLSDNEEWSLQAVEKHTLVALKRVQ	ALQOQRESSVAPETONPPEAA	214
Qy	194	GQKGGVAYTNQDRKITQLCGELYDLDASSLQLKVLQYL	QOQETQASRCCLLLVSDNLQL	253
Db	215	GQKGGVAYTDQDRKITQLCGELYDLDASSLQLKVLQYL	QOQETQASRCCLLLVSDNLQL	274
Qy	254	SCKVIGDKVLEBESIFPLTTGRLGQVVEDKKSQIKDLT	SDMQQLQSMGCEVOAMLCV	313
Db	275	SCKVIGDKVLEBESIFPLTTGRLGQVVEDKKSQIKDLT	SDMQQLQSMGCEVOAMLCV	334
Qy	314	PVISRATQVVALACAFNKLGGDLTDQDEHVIQHC	FHYTSTVLSTLAFQKEQKLKCEC	373
Db	335	PVISRATQVVALACAFNKLGGDLTDQDEHVIQHC	FHYTSTVLSTLAFQKEQKLKCEC	394
Qy	374	QALLQVAKNLFTHLDDVSVLLQEIITEARNLSNAEICS	VFLDDQNELVAKVFDGGVDE	433
Db	395	QALLQVAKNLFTHLDDVSVLLQEIITEARNLSNAEICS	VFLDDQNELVAKVFDGGVDE	454
Qy	434	SYEIRIPADQGIAGHVAATTGQILNIPDAYAHP	PLFYRGVDDSTGFRTRNLCFPIKNQOE	493
Db	455	SYEIRIPADQGIAGHVAATTGQILNIPDAYAHP	PLFYRGVDDSTGFRTRNLCFPIKNQOE	514
Qy	494	VIGVAELVNKINGPWFSPFDEDLATAFSIYCGISIAH	SLLYKKVNEAQYRSHLANEMMY	553
Db	515	VIGVAELVNKINGPWFSPFDEDLATAFSIYCGISIAH	SLLYKKVNEAQYRSHLANEMMY	574

Qy	554	HKVSDDEYTKLLHDGIQPVAADSNFASFTYTPRSLPEDD	TSMALLSMLQDMNFNNYK	613
Db	575	HKVSDDEYTKLLHDGIQPVAADSNFASFTYTPRSLPEDD	TSMALLSMLQDMNFNNYK	634
Qy	614	IDCPTLARFCLMVKKGYRDPVYHNMHAFSVSHFCVLLY	KNLELNTYLEDMEIFALFISC	673
Db	635	IDCPTLARFCLMVKKGYRDPVYHNMHAFSVSHFCVLLY	KNLELNTYLEDMEIFALFISC	694
Qy	674	MCHDLDRGTNNNSFQVASKSVLAALYSSEGSVMERHFA	QAIAIANTHGCNIFDHFSRKD	733
Db	695	MCHDLDRGTNNNSFQVASKSVLAALYSSEGSVMERHFA	QAIAIANTHGCNIFDHFSRKD	754
Qy	734	YQMLDLMRDIILATDLAHLRIIPKDLQMAEVGYDRTN	KQHSLLLCLLMTSCDLSDT	793
Db	755	YQMLDLMRDIILATDLAHLRIIPKDLQMAEVGYDRTN	KQHSLLLCLLMTSCDLSDT	814
Qy	794	KGMKTRKIAELIYKEFFSQGDLEKAMGNRPMEMMDRE	KAYIPELQISFMEHIAMPIYKL	853
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Qy	854	LQDLFPKAAELYERVAENREHWTKVSHKFTIRGLPSN	NSLDFLDBEYEVPLDGGARAPIN	913
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Qy	914	GCCSLDAE	921	
Db	935	GCCSLDAE	942	

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OM protein - protein search, using sw model

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3087.987 Million cell updates/sec

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Perfect score: 4781  
Sequence: 1 MRQPAASDLFAQEPVPG.....VFDLGARAPINGCCSLDAS 921

Scoring table: BLOSUM62  
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Searched: 1717557 seqs, 384547976 residues

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Post-processing: Minimum Match 0%  
Maximum Match 100%  
Listing first 45 summaries

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17: /cgn2\_6/ptodata/2/pubpaa/US10E\_PUBCOMB.pep.\*  
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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

#### SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	4781	100.0	921	9 US-09-883-825-39	Sequence 39, Appl
2	4781	100.0	921	13 US-10-094-989-5	Sequence 5, Appl
3	4781	100.0	921	16 US-10-697-894-39	Sequence 39, Appl
4	4657	97.4	942	9 US-09-883-825-43	Sequence 43, Appl
5	4657	97.4	942	16 US-10-697-894-43	Sequence 43, Appl
6	4539.5	94.9	920	15 US-10-236-417-78	Sequence 78, Appl
7	4533.5	94.8	920	13 US-10-094-989-2	Sequence 2, Appl
8	4474.5	93.6	941	9 US-09-883-825-45	Sequence 45, Appl
9	4474.5	93.6	941	16 US-10-697-894-45	Sequence 45, Appl
10	4474.5	93.6	941	16 US-10-686-390-5	Sequence 5, Appl
11	4474.5	93.6	941	17 US-10-686-282-5	Sequence 5, Appl

12	4474.5	93.6	941	17	US-10-686-349-5	Sequence 5, Appl
13	4473.5	93.6	905	13	US-10-094-989-4	Sequence 4, Appl
14	4148.5	86.8	950	15	US-10-108-260A-2928	Sequence 2928, Ap
15	3543.5	74.1	786	15	US-10-104-047-2944	Sequence 2944, Ap
16	1766	36.9	334	17	US-10-771-833-30	Sequence 30, Appl
17	1766	36.9	334	17	US-10-886-949-30	Sequence 30, Appl
18	991	20.7	934	9	US-09-891-216-12	Sequence 12, Appl
19	991	20.7	934	9	US-09-891-216-15	Sequence 15, Appl
20	991	20.7	934	14	US-10-168-402-2	Sequence 2, Appl
21	983	20.6	1284	14	US-10-296-144-5	Sequence 5, Appl
22	974.5	20.4	934	14	US-10-168-402-39	Sequence 39, Appl
23	920.5	19.3	684	9	US-09-891-216-14	Sequence 14, Appl
24	920.5	19.3	684	14	US-10-168-402-4	Sequence 4, Appl
25	920.5	19.3	684	16	US-10-746-197-1	Sequence 1, Appl
26	914.5	19.1	779	9	US-09-420-190-1	Sequence 1, Appl
27	914.5	19.1	779	15	US-10-458-839-1	Sequence 1, Appl
28	914.5	19.1	779	15	US-10-440-998-6	Sequence 6, Appl
29	914	19.1	789	9	US-09-321-801-2	Sequence 2, Appl
30	914	19.1	789	15	US-10-618-252-2	Sequence 2, Appl
31	913	19.1	803	15	US-10-440-998-4	Sequence 4, Appl
32	912.5	19.1	766	15	US-10-440-998-2	Sequence 2, Appl
33	912.5	19.1	791	9	US-09-321-801-4	Sequence 4, Appl
34	912.5	19.1	791	15	US-10-618-252-4	Sequence 4, Appl
35	909	19.0	796	9	US-09-321-801-15	Sequence 15, Appl
36	909	19.0	796	15	US-10-618-252-15	Sequence 15, Appl
37	892	18.7	684	14	US-10-168-402-6	Sequence 6, Appl
38	887	18.6	773	14	US-10-202-107-2	Sequence 2, Appl
39	887	18.6	773	17	US-10-887-276-2	Sequence 2, Appl
40	845.5	17.7	576	9	US-09-891-216-13	Sequence 13, Appl
41	845.5	17.7	576	16	US-10-746-197-3	Sequence 3, Appl
42	801	16.8	874	15	US-10-427-222-3	Sequence 3, Appl
43	801	16.8	875	14	US-10-115-515-23	Sequence 23, Appl
44	801	16.8	875	14	US-10-094-168B-5	Sequence 5, Appl
45	801	16.8	875	17	US-10-771-833-1	Sequence 1, Appl

#### ALIGNMENTS

#### RESULT 1

US-09-883-825-39  
; Sequence 39, Application US/09883825  
; Patent No. US20020151024A1  
; GENERAL INFORMATION:  
; APPLICANT: Beavo, Joseph A.  
; Bentley, Kelley  
; Charbonneau, Harry  
; Sonnenburg, William K.  
; TITLE OF INVENTION: DNA Encoding Mammalian  
; Phosphodiesterases  
; NUMBER OF SEQUENCES: 58  
; CORRESPONDENCE ADDRESS:  
; ADDRESSEE: Marshall, O'Toole, Gerstein, Murray &  
; STREET: Two First National Plaza, 20 South Clark  
; Bicknell  
; Street  
; CITY: Chicago  
; STATE: Illinois  
; COUNTRY: USA  
; ZIP: 60603  
; COMPUTER READABLE FORM:  
; MEDIUM TYPE: Floppy disk  
; COMPUTER: IBM PC compatible  
; OPERATING SYSTEM: PC-DOS/MS-DOS  
; SOFTWARE: PatentIn Release #1.0, Version #1.25  
; CURRENT APPLICATION DATA:  
; APPLICATION NUMBER: US/09/883,825  
; FILING DATE: 18-Jun-2001  
; CLASSIFICATION: <Unknown>  
; PRIOR APPLICATION DATA:  
; APPLICATION NUMBER: 09/123,783  
; FILING DATE: <Unknown>  
; APPLICATION NUMBER: 08/297,494



481 NILCPPIKNEQVIGVAGELVKNKINGPWFSPKDEDLATAFSYCGISIAHSLLYKKVNEA 540  
481 NILCPPIKNEQVIGVAGELVKNKINGPWFSPKDEDLATAFSYCGISIAHSLLYKKVNEA 540  
541 QYRSHLANEMMYHMKVSDDEYTKLLHDGIPQVAAIDSNFASFTYTPRSLPDDTSMALL 600  
541 QYRSHLANEMMYHMKVSDDEYTKLLHDGIPQVAAIDSNFASFTYTPRSLPDDTSMALL 600  
601 SMLQDMNFNNYKIDCPTLARFCLMVKKGGRDPPYHNNMHAFSVSHFCYLLYKNLELTYNY 660  
601 SMLQDMNFNNYKIDCPTLARFCLMVKKGGRDPPYHNNMHAFSVSHFCYLLYKNLELTYNY 660  
661 LEDMEIFALFISCMCHDLDRGTNNNSFQVASKSVLAALYSSEGSVNERHHFPAQAIANT 720  
661 LEDMEIFALFISCMCHDLDRGTNNNSFQVASKSVLAALYSSEGSVNERHHFPAQAIANT 720  
721 HGCNIFDHFSSRKYQRMOLDLMDRIILATDLAHLRIFKDLQKMAEYGYDRTNKHSHLL 780  
721 HGCNIFDHFSSRKYQRMOLDLMDRIILATDLAHLRIFKDLQKMAEYGYDRTNKHSHLL 780  
781 CLMTSCDLSDOTKGWTKTRKIAELIYKEFFSQGDLKAMGNRPWEMMDREKAYIPELOI 840  
781 CLMTSCDLSDOTKGWTKTRKIAELIYKEFFSQGDLKAMGNRPWEMMDREKAYIPELOI 840  
841 SPWEHIAMPIYKLLQDLFPKAAELYERVAENREHMTKVSHTTIRGLPSNNSLDFDEY 900  
841 SPWEHIAMPIYKLLQDLFPKAAELYERVAENREHMTKVSHTTIRGLPSNNSLDFDEY 900  
901 EYVDLDGARAPINGCCSLDAE 921  
901 EYVDLDGARAPINGCCSLDAE 921

RESULT 3

US-10-697-894-39  
Sequence 39, Application US/10697894  
Publication NO. US2004012686A1  
GENERAL INFORMATION:  
APPLICANT: Beavo, Joseph A.  
Bentley, Kelley  
Charbonneau, Harry  
Sonnenburg, William K.  
TITLE OF INVENTION: DNA Encoding Mammalian  
Phosphodiesterases  
NUMBER OF SEQUENCES: 58  
CORRESPONDENCE ADDRESS:  
ADDRESSEE: Marshall, O'Toole, Gerstein, Murray &  
Bicknell  
Street  
Two First National Plaza, 20 South Clark  
City: Chicago  
State: Illinois  
Country: USA  
ZIP: 60603  
COMPUTER READABLE FORM:  
MEDIUM TYPE: Floppy disk  
COMPUTER: IBM PC compatible  
OPERATING SYSTEM: PC-DOS/MS-DOS  
SOFTWARE: PatentIn Release #1.0, Version #1.25  
CURRENT APPLICATION NUMBER: US/10/697,894  
FILING DATE: 30-Oct-2003  
CLASSIFICATION: <Unknown>  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: US/09/123,783  
FILING DATE: 28-July-1998  
APPLICATION NUMBER: 08/297,494  
FILING DATE: <Unknown>  
APPLICATION NUMBER: US 07/688,356  
FILING DATE: 04-APR-1991  
ATTORNEY/AGENT INFORMATION:  
NAME: Noland, Greta E.

REGISTRATION NUMBER: 35,302  
REFERENCE/DOCKET NUMBER: 27866/30822  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: (312) 346-5750  
TELEFAX: (312) 984-9740  
TELEX: 25-3856  
INFORMATION FOR SEQ ID NO: 39:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 921 amino acids  
TYPE: amino acid  
TOPOLOGY: linear  
MOLECULE TYPE: protein  
SEQUENCE DESCRIPTION: SEQ ID NO: 39:  
US-10-697-894-39

Query Match 100.0%; Score 4781; DB 16; Length 921;  
Best Local Similarity 100.0%; Pred. No. 0;  
Matches 921; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
QY 1 MRRQPAASRDLPFAQBPVPPGSGDGLADALLSLGSLVTVAGLQQAQVKEALSAPLKVETV 60  
Db 1 MRRQPAASRDLPFAQBPVPPGSGDGLADALLSLGSLVTVAGLQQAQVKEALSAPLKVETV 60  
QY 61 YTYLLDGSRLVCEPPELPOEGKVRVAVISRKLGCGNLGSPDLPGKPLARLVAPLAP 120  
Db 61 YTYLLDGSRLVCEPPELPOEGKVRVAVISRKLGCGNLGSPDLPGKPLARLVAPLAP 120  
QY 121 DTQVLVILPLVKEAGAAVAILVHCGQLSDNEWSLQAVEKHITLVALKEVQALQOQRESSV 180  
Db 121 DTQVLVILPLVKEAGAAVAILVHCGQLSDNEWSLQAVEKHITLVALKEVQALQOQRESSV 180  
QY 181 APEATONPPEAAGDQKGVAYTNQDKILQICGELYDLDASSLQIKVLYLOQETQASR 240  
Db 181 APEATONPPEAAGDQKGVAYTNQDKILQICGELYDLDASSLQIKVLYLOQETQASR 240  
QY 241 CCLLVSEDNQLSCKVIGDKVLEEEISFPLTTGRLGQVVEDEKSTOLKDLTSEDQQQLQ 300  
Db 241 CCLLVSEDNQLSCKVIGDKVLEEEISFPLTTGRLGQVVEDEKSTOLKDLTSEDQQQLQ 300  
QY 301 SMLGCEVQAMLCVVISRATDOVALACAFNKGGLDFTDQDEHVIQCHFYHTSTVLTST 360  
Db 301 SMLGCEVQAMLCVVISRATDOVALACAFNKGGLDFTDQDEHVIQCHFYHTSTVLTST 360  
QY 361 LAFQKEQKLKCEQALQVAKNLFTHLDDVSVLLQEIITEARNLSNAEICSFVLLDQNEL 420  
Db 361 LAFQKEQKLKCEQALQVAKNLFTHLDDVSVLLQEIITEARNLSNAEICSFVLLDQNEL 420  
QY 421 VAKVPDGGVVEDESEYIRIPADQGIAGHVATTGQILNIPDAYAHPLFYRGVDDSTGFRTR 480  
Db 421 VAKVPDGGVVEDESEYIRIPADQGIAGHVATTGQILNIPDAYAHPLFYRGVDDSTGFRTR 480  
QY 481 NILCPPIKNEQVIGVAGELVKNKINGPWFSPKDEDLATAFSYCGISIAHSLLYKKVNEA 540  
Db 481 NILCPPIKNEQVIGVAGELVKNKINGPWFSPKDEDLATAFSYCGISIAHSLLYKKVNEA 540  
QY 541 QYRSHLANEMMYHMKVSDDEYTKLLHDGIPQVAAIDSNFASFTYTPRSLPDDTSMALL 600  
Db 541 QYRSHLANEMMYHMKVSDDEYTKLLHDGIPQVAAIDSNFASFTYTPRSLPDDTSMALL 600  
QY 601 SMLQDMNFNNYKIDCPTLARFCLMVKKGGRDPPYHNNMHAFSVSHFCYLLYKNLELTYNY 660  
Db 601 SMLQDMNFNNYKIDCPTLARFCLMVKKGGRDPPYHNNMHAFSVSHFCYLLYKNLELTYNY 660  
QY 661 LEDMEIFALFISCMCHDLDRGTNNNSFQVASKSVLAALYSSEGSVNERHHFPAQAIANT 720  
Db 661 LEDMEIFALFISCMCHDLDRGTNNNSFQVASKSVLAALYSSEGSVNERHHFPAQAIANT 720  
QY 721 HGCNIFDHFSSRKYQRMOLDLMDRIILATDLAHLRIFKDLQKMAEYGYDRTNKHSHLL 780  
Db 721 HGCNIFDHFSSRKYQRMOLDLMDRIILATDLAHLRIFKDLQKMAEYGYDRTNKHSHLL 780  
QY 781 CLMTSCDLSDOTKGWTKTRKIAELIYKEFFSQGDLKAMGNRPWEMMDREKAYIPELOI 840  
Db 781 CLMTSCDLSDOTKGWTKTRKIAELIYKEFFSQGDLKAMGNRPWEMMDREKAYIPELOI 840

Db 781 CILMTSCDLSQDTGKWKTRTKIAELIYKEFFSQGLEKAMGNRPMMMDREKAYIPELQI 840  
Qy 841 SFMEHIAMPIYKLLQDLPEKAAELYERVAENREHWTKVSHKFTIRGLPSNNSLDFLDEEY 900  
Db 841 SFMEHIAMPIYKLLQDLPEKAAELYERVAENREHWTKVSHKFTIRGLPSNNSLDFLDEEY 900  
Qy 901 EVPDLGAPINGGCCSLDAE 921  
Db 901 EVPDLGAPINGGCCSLDAE 921

## RESULT 4

US-09-883-825-43  
; Sequence 43, Application US/09883825  
; Patent No. US20020151024A1  
; GENERAL INFORMATION:  
; APPLICANT: Beavo, Joseph A.  
; Bentley, Kelley  
; Charbonneau, Harry  
; Sonnenburg, William K.  
; TITLE OF INVENTION: DNA Encoding Mammalian  
; Phosphodiesterases  
; NUMBER OF SEQUENCES: 58  
; CORRESPONDENCE ADDRESS:  
; ADDRESSEE: Marshall, O'Toole, Gerstein, Murray &  
; Bicknell  
; STREET: Two First National Plaza, 20 South Clark  
; Street  
; CITY: Chicago  
; STATE: Illinois  
; COUNTRY: USA  
; ZIP: 60603

COMPUTER READABLE FORM:  
; MEDIUM TYPE: Floppy disk  
; COMPUTER: IBM PC compatible  
; OPERATING SYSTEM: PC-DOS/MS-DOS  
; SOFTWARE: Patent In Release #1.0, Version #1.25  
; CURRENT APPLICATION DATA:  
; APPLICATION NUMBER: US/09/883,825  
; FILING DATE: 18-Jun-2001  
; CLASSIFICATION: <Unknown>  
; PRIOR APPLICATION DATA:  
; APPLICATION NUMBER: 09/123,783  
; FILING DATE: <Unknown>  
; APPLICATION NUMBER: 08/297,494  
; FILING DATE: <Unknown>  
; APPLICATION NUMBER: US 07/688,356  
; FILING DATE: 04-APR-1991

ATTORNEY/AGENT INFORMATION:  
; NAME: No. US20020151024A1and, Greta E.  
; REGISTRATION NUMBER: 35,302  
; REFERENCE/DOCKET NUMBER: 27866/30822  
; TELECOMMUNICATION INFORMATION:  
; TELEPHONE: (312) 346-5750  
; TELEFAX: (312) 984-9740  
; TELEX: 25-3856

INFORMATION FOR SEQ ID NO: 43:  
; SEQUENCE CHARACTERISTICS:  
; LENGTH: 942 amino acids  
; TYPE: amino acid  
; TOPOLOGY: linear  
; MOLECULE TYPE: protein  
; SEQUENCE DESCRIPTION: SEQ ID NO: 43:

US-09-883-825-43  
Query Match 97.4%; Score 4657; DB 9; Length 942;  
Best Local Similarity 98.9%; Pred. No. 0;  
Matches 898; Conservative 3; Mismatches 7; Indels 0; Gaps 0;  
Qy 14 QEPVPPGSGDALQDALLSLGSDVIDAGLQAAVKALSAVLPKVETVTVYLLDGESRLVC 73  
Db 35 EPPPPPPQCADSLQDALLSLGSDVIDAGLQAAVKALSAVLPKVETVTVYLLDGESRLVC 94

Qy 74 BEPPHELPOEGKREAVISRKRLGNGLGPSPDLPGKPLARLVAPLAPDPTQVLVPLVDKE 133  
Db 95 BEPPHELPOEGKREAVISRKRLGNGLGPSPDLPGKPLARLVAPLAPDPTQVLVPLVDKE 154  
Qy 134 AGAAVAAILVHCQGLSDNEEWSLQAVEKHTLVALKRVOALQOORESSVAPEATQNPPEAA 193  
Db 155 AGAAVAAILVHCQGLSDNEEWSLQAVEKHTLVALKRVOALQOORESSVAPEATQNPPEAA 214  
Qy 194 GDQGGVAYTMDRKILQLCGELYDLDAASSLQVLQYLOQETOASRCCLLLVSDNLQ 253  
Db 215 GDQGGVAYTMDRKILQLCGELYDLDAASSLQVLQYLOQETOASRCCLLLVSDNLQ 274  
Qy 254 SKVIGDKVLEEEISFPITTRGLQGVVEDKKSIIQLKDLTSDMQLOQSMGLCEVQAMLCV 313  
Db 275 SKVIGDKVLEEEISFPITTRGLQGVVEDKKSIIQLKDLTSDMQLOQSMGLCEVQAMLCV 334  
Qy 314 PVISRATDQVVALACAFNKLGGDLFTDQDEHVIQHCFFHYTSTVLTSTLAPQKEQKLKCEC 373  
Db 335 PVISRATDQVVALACAFNKLGGDLFTDQDEHVIQHCFFHYTSTVLTSTLAPQKEQKLKCEC 394  
Qy 374 QALLQVAKNLFTHLDVSVLLQEIITEARNLSNAEICSVFLLDQNELVAKVDFDGVVDE 433  
Db 395 QALLQVAKNLFTHLDVSVLLQEIITEARNLSNAEICSVFLLDQNELVAKVDFDGVVDE 454  
Qy 434 SYEIRIPADQGIAGHVATTGOILNIPDAYAHPFYRGVDDSTGFRTRNLCFFPKENQOE 493  
Db 455 SYEIRIPADQGIAGHVATTGOILNIPDAYAHPFYRGVDDSTGFRTRNLCFFPKENQOE 514  
Qy 494 VIGVAELVNKINGPWFPSKFDDELATAFSIYCGISIAHSLLYKVNIAQYRSHLANEMMY 553  
Db 515 VIGVAELVNKINGPWFPSKFDDELATAFSIYCGISIAHSLLYKVNIAQYRSHLANEMMY 574  
Qy 554 HMKVSDDEYTKLLHDGIQPVAAIDSNFASPTTTPRSLPEDDTSMALLSMLQDMNFINNYK 613  
Db 575 HMKVSDDEYTKLLHDGIQPVAAIDSNFASPTTTPRSLPEDDTSMALLSMLQDMNFINNYK 634  
Qy 614 IDCPTLARFCLMWKGYRDPYPHNMHAFSVSHFCYLLYKXLELTNYLEDMEIPALFTSC 673  
Db 635 IDCPTLARFCLMWKGYRDPYPHNMHAFSVSHFCYLLYKXLELTNYLEDMEIPALFTSC 694  
Qy 674 MCHDLDRGTNNSFQVASKSVLAALYSSEGSMERHHFAQAIALNTHGNCNIFDHSRKD 733  
Db 695 MCHDLDRGTNNSFQVASKSVLAALYSSEGSMERHHFAQAIALNTHGNCNIFDHSRKD 754  
Qy 734 YQRMIDLMDRIILATDLAHLRIFKDLQKMAEVGYDRTNKHSHLLCLLMTSCDLSDOT 793  
Db 755 YQRMIDLMDRIILATDLAHLRIFKDLQKMAEVGYDRTNKHSHLLCLLMTSCDLSDOT 814  
Qy 794 KGWKTTRKIAELIYKEFFSQGLEKAMGNRPMMMDREKAYIPELQISFMHIAMPIYKL 853  
Db 815 KGWKTTRKIAELIYKEFFSQGLEKAMGNRPMMMDREKAYIPELQISFMHIAMPIYKL 874  
Qy 854 LQDLFPKAAELYERVAENREHWTKVSHKFTIRGLPSNNSLDFLDEEVEVPDLGAPIN 913  
Db 875 LQDLFPKAAELYERVAENREHWTKVSHKFTIRGLPSNNSLDFLDEEVEVPDLGAPIN 934  
Qy 914 GCCSLDAE 921  
Db 935 GCCSLDAE 942

## RESULT 5

US-10-697-894-43  
; Sequence 43, Application US/10697894  
; Publication No. US20040126866A1  
; GENERAL INFORMATION:  
; APPLICANT: Beavo, Joseph A.  
; Bentley, Kelley  
; Charbonneau, Harry  
; Sonnenburg, William K.  
; TITLE OF INVENTION: DNA Encoding Mammalian  
; Phosphodiesterases  
; NUMBER OF SEQUENCES: 58

;; CORRESPONDENCE ADDRESS:  
;; ADDRESSEE: Marshall, O'Toole, Gerstein, Murray &  
;; Bicknell  
;; STREET: Two First National Plaza, 20 South Clark  
;; Street  
;; CITY: Chicago  
;; STATE: Illinois  
;; COUNTRY: USA  
;; ZIP: 60603  
;;  
;; COMPUTER READABLE FORM:  
;; MEDIUM TYPE: Floppy disk  
;; COMPUTER: IBM PC compatible  
;; OPERATING SYSTEM: PC-DOS/MS-DOS  
;; SOFTWARE: Patent In Release #1.0, Version #1.25  
;; CURRENT APPLICATION DATA:  
;; APPLICATION NUMBER: US/10/697,894  
;; FILING DATE: 30-Oct-2003  
;; CLASSIFICATION: <Unknown>  
;; PRIOR APPLICATION DATA:  
;; APPLICATION NUMBER: US/09/123,783  
;; FILING DATE: 28-July-1998  
;; APPLICATION NUMBER: 08/297,494  
;; FILING DATE: <Unknown>  
;; APPLICATION NUMBER: US 07/688,356  
;; FILING DATE: 04-APR-1991  
;; ATTORNEY/AGENT INFORMATION:  
;; NAME: Noland, Greta E.  
;; REGISTRATION NUMBER: 35,302  
;; REFERENCE/DOCKET NUMBER: 27866/30822  
;; TELECOMMUNICATION INFORMATION:  
;; TELEPHONE: (312) 346-5750  
;; TELEFAX: (312) 984-9740  
;; TELEX: 25-3856  
;; INFORMATION FOR SEQ ID NO: 43:  
;; SEQUENCE CHARACTERISTICS:  
;; LENGTH: 942 amino acids  
;; TYPE: amino acid  
;; TOPOLOGY: linear  
;; MOLECULE TYPE: protein  
;; SEQUENCE DESCRIPTION: SEQ ID NO: 43:  
US-10-697-894-43

Query Match 97.4%; Score 4657; DB 16; Length 942;  
Best Local Similarity 98.9%; Pred. No. 0;  
Matches 898; Conservative 3; Mismatches 7; Indels 0; Gaps 0;

QY 14 QEPVPGSGDGLQDALLSLGSDVIDVAGLQQAQKALSAVLPKVETVYTYLLDGSRLVC 73  
Db 35 EPPPPPPQCADSLQDALLSLGSDVIDVAGLQQAQKALSAVLPKVETVYTYLLDGSRLVC 94  
QY 74 BEPPHELPOEGKVRBAVSRKRLGCGNGLGSPDLPGKPLARLVAPLAPDTQVLVPLVDKE 133  
Db 95 BEPPHELPOEGKVRBAVSRKRLGCGNGLGSPDLPGKPLARLVAPLAPDTQVLVPLVDKE 154  
QY 134 AGAAVAATLVHCGQLSDNEEWSLQAVEKHTLVALKRVQALQORESSVAPEATQNPBAAA 193  
Db 155 AGAAVAATLVHCGQLSDNEEWSLQAVEKHTLVALKRVQALQORESSVAPEATQNPBAAA 214  
QY 194 GDQKGGVATWDRKILQICGELYDLDAASSLQKLVQLQOETQASRCCLLVSDNLQL 253  
Db 215 GDQKGGVATWDRKILQICGELYDLDAASSLQKLVQLQOETQASRCCLLVSDNLQL 274  
QY 254 SKCVIGDKVLEEEISFPITTRGLRGQVDEKKSQIKDLTSDMQQLQSMGCEVQAMLCV 313  
Db 275 SKCVIGDKVLEEEISFPITTRGLRGQVDEKKSQIKDLTSDMQQLQSMGCEVQAMLCV 334  
QY 314 PVISRATQWVALACAFNKLGGDLFTDQDHEVHQHCFHYTSTVLSTFLAFQKEQKLKCEC 373  
Db 335 PVISRATQWVALACAFNKLGGDLFTDQDHEVHQHCFHYTSTVLSTFLAFQKEQKLKCEC 394  
QY 374 QALLOVAKNLFTHLDDVSVLQEIITEARNLSNABICSVFLDDQNELVAKVPDGGVDEDE 433  
Db 395 QALLOVAKNLFTHLDDVSVLQEIITEARNLSNABICSVFLDDQNELVAKVPDGGVDEDE 454

QY 434 SYEIRIPADQGIAGHVATTGQILNIPDAYAHPLFYRGVDDSTGFRTRNLCPPKINNOE 493  
Db 455 SYEIRIPADQGIAGHVATTGQILNIPDAYAHPLFYRGVDDSTGFRTRNLCPPKINNOE 514  
QY 494 VIGVAELVKNKINGPWFSPKDEDLATAFSIYCGISIAHSLLYKKVNEAQYRSHLANEMMY 553  
Db 515 VIGVAELVKNKINGPWFSPKDEDLATAFSIYCGISIAHSLLYKKVNEAQYRSHLANEMMY 574  
QY 554 HMKVSDDEYTKLLHDGIQPVAAIDSNFASFTYTPRSLPEDDTSMALLMLQDMNFINNYK 613  
Db 575 HMKVSDDEYTKLLHDGIQPVAAIDSNFASFTYTPRSLPEDDTSMALLMLQDMNFINNYK 634  
QY 614 IDCPTLARFCLMVKKGYRDPYPVNNMHAFPSVSHFCVLLYKNLELTYLDEMEIFALFISC 673  
Db 635 IDCPTLARFCLMVKKGYRDPYPVNNMHAFPSVSHFCVLLYKNLELTYLDEMEIFALFISC 694  
QY 674 MCHDLDRHGTNNSFOVASKSVLAALYSSEGVSWEHRHFAQATAILNTHCGNIPDFHSRKD 733  
Db 695 MCHDLDRHGTNNSFOVASKSVLAALYSSEGVSWEHRHFAQATAILNTHCGNIPDFHSRKD 754  
QY 734 YQMLDLMRDIIATDLAHLRIFKDLQMAEVGYDRTNKHSHLLCLLMTSCDLSQDT 793  
Db 755 YQMLDLMRDIIATDLAHLRIFKDLQMAEVGYDRTNKHSHLLCLLMTSCDLSQDT 814  
QY 794 KGWKTTRKIAELIYKEFFSQGDLEKAMGNRPMEMDREKAYIPELQISPMEHIAPIYKL 853  
Db 815 KGWKTTRKIAELIYKEFFSQGDLEKAMGNRPMEMDREKAYIPELQISPMEHIAPIYKL 874  
QY 854 LODLFPKAAELYERVASNRHWTKYSHKFTIRGLSNNSLDPLDEYEVDPDLGAPIN 913  
Db 875 LODLFPKAAELYERVASNRHWTKYSHKFTIRGLSNNSLDPLDEYEVDPDLGAPIN 934  
QY 914 GCCSLDAE 921  
Db 935 GCCSLDAE 942

## RESULT 6

US-10-236-417-78  
; Sequence 78, Application US/10236417  
; Publication No. US20040048256A1  
; GENERAL INFORMATION:  
; APPLICANT: Agee et al.  
; TITLE OF INVENTION: NOVEL PROTEINS AND NUCLEIC ACIDS ENCODING SAME  
; FILE REFERENCE: 21402-442C  
; CURRENT APPLICATION NUMBER: US/10/236,417  
; CURRENT FILING DATE: 2003-01-06  
; PRIOR APPLICATION NUMBER: US60/318,120  
; PRIOR FILING DATE: 2001-09-01  
; PRIOR APPLICATION NUMBER: US60/318,430  
; PRIOR FILING DATE: 2001-09-10  
; PRIOR APPLICATION NUMBER: US60/322,781  
; PRIOR FILING DATE: 2001-09-17  
; PRIOR APPLICATION NUMBER: US60/318,184  
; PRIOR FILING DATE: 2001-09-07  
; PRIOR APPLICATION NUMBER: US60/361,663  
; PRIOR FILING DATE: 2002-03-05  
; PRIOR APPLICATION NUMBER: US60/396,412  
; PRIOR FILING DATE: 2002-07-17  
; PRIOR APPLICATION NUMBER: US60/322,636  
; PRIOR FILING DATE: 2001-09-17  
; PRIOR APPLICATION NUMBER: US60/322,817  
; PRIOR FILING DATE: 2001-09-17  
; PRIOR APPLICATION NUMBER: US60/322,816  
; PRIOR FILING DATE: 2001-09-17  
; PRIOR APPLICATION NUMBER: US60/323,519  
; PRIOR FILING DATE: 2001-09-19  
; Remaining Prior Application data removed - See File Wrapper or PALM.  
; NUMBER OF SEQ ID NOS: 341  
; SOFTWARE: Custom  
; SEQ ID NO 78  
; LENGTH: 920









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; PRIOR FILING DATE: 2000-03-29
; PRIOR APPLICATION NUMBER: US 60/217,479
; PRIOR FILING DATE: 2000-07-11
; PRIOR APPLICATION NUMBER: US 60/221,014
; PRIOR FILING DATE: 2000-07-27
; Remaining Prior Application data removed - See File Wrapper or PALM.
; NUMBER OF SEQ ID NOS: 20
; SOFTWARE: PatentIn version 3.2
; SEQ ID NO 5
; LENGTH: 941
; TYPE: PRT
; ORGANISM: Homo Sapiens
US-10-686-390-5

Query Match          93.6%; Score 4474.5; DB 16; Length 941;
Best Local Similarity 94.7%; Pred. No. 0;
Matches 860; Conservative 21; Mismatches 26; Indels 1; Gaps 1;

QY 14 QBPVPPGSGDALQDALLSLGSDVIDVAGLQQAQVKEALSAVLPKVTYTYLLDGSRLVC 73
DB 35 EPPPPQPCADSLQDALLSLGSDVIDISGLQRAVKEALSAVLPKVTYTYLLDGSRLVC 94
QY 74 EPPHLPQEGKREAVISRKRLGCGNGLGFSPLPGKPLARLVAPLAPDTQVLPVLDKE 133
DB 95 EPPHLPQEGKREAVISRKRLGCGNGLGFSPLPGKPLARLVAPLAPDTQVLPVLDKE 154
QY 134 AGAAVAVILVHCGQLSDNEEWSLQAVKHTLVALKRVQALQOQRESSVAPEATQNPPEAA 193
DB 155 AGAAVAVILVHCGQLSDNEEWSLQAVKHTLVALKRVQALQOQRESSVAPEATQNPPEAA 214
QY 194 GQKGGVATNDRKILQICGELYDLDASSLQKVLQYLQOQTRASRCCLLLVSEDLQL 253
DB 215 EDQKGGAAVTRDRKILQICGELYDLDASSLQKVLQYLQOQTRASRCCLLLVSEDLQL 274
QY 254 SKCVIGDKVLEBEISPLTTRGRLQGVVEDKKSITQLKDLTSEDQQQLQSMGCEVQAMLCV 313
DB 275 SKCVIGDKVLEBEISPLTTRGRLQGVVEDKKSITQLKDLTSEDQQQLQSMGCEVQAMLCV 333
QY 314 PVISRATQDVALACAFNKLGGDLFTDDEHVIQHCFTYTSVLTSTLAFQEKQLKRCB 373
DB 334 PVISRATQDVALACAFNKLGGDLFTDDEHVIQHCFTYTSVLTSTLAFQEKQLKRCB 393
QY 374 QALLQVAKNLFTHLDDVSVLLQEIITEARNLSNAEICSVFLLDQNELVAKVDFGCVDE 433
DB 394 QALLQVAKNLFTHLDDVSVLLQEIITEARNLSNAEICSVFLLDQNELVAKVDFGCVDE 453
QY 434 SYEIRIPADQGTAGHVATTGQILNTPDAYAHPLFYRGVDDSTGFRTRNLCFPIKXNQE 493
DB 454 SYEIRIPADQGTAGHVATTGQILNTPDAYAHPLFYRGVDDSTGFRTRNLCFPIKXNQE 513
QY 494 VIGVAELVNKINGPFSKPEDDLATAFSYCGISIAHSLLYKKVNEAQYRSHLANEMMY 553
DB 514 VIGVAELVNKINGPFSKPEDDLATAFSYCGISIAHSLLYKKVNEAQYRSHLANEMMY 573
QY 554 HMKVSDDEVTKLLHDCIQVAIDSNFASFTYTPRSLPEDDTSMALLSMLQDMNFNNYK 613
DB 574 HMKVSDDEVTKLLHDCIQVAIDSNFASFTYTPRSLPEDDTSMALLSMLQDMNFNNYK 633
QY 614 IDCPTLARECLMVKGYRPPPHNNWHAESVSHFCYLLYKNLELYNLEIMEIFALFISC 673
DB 634 IDCPTLARECLMVKGYRPPPHNNWHAESVSHFCYLLYKNLELYNLEIMEIFALFISC 693
QY 674 MCHDLDRHTNNSFOVAKSVLAALYSSEGSVWERHHFAQAIATLINTHGCNIPDFHSRKO 733
DB 694 MCHDLDRHTNNSFOVAKSVLAALYSSEGSVWERHHFAQAIATLINTHGCNIPDFHSRKO 753
QY 734 YQRMOLDLMDRIIATDLAHLRI PKDLQKVAEYGVYDRNTKQHSLLLCLLMTSCDLSQDT 793
DB 754 YQRMOLDLMDRIIATDLAHLRI PKDLQKVAEYGVYDRNTKQHSLLLCLLMTSCDLSQDT 813
QY 794 KGWKTTRKIAELIYKEFFSQGDLKAMGNRPNEMMDREKAYIPELQISFMEHIANPIYKL 853
DB 814 KGWKTTRKIAELIYKEFFSQGDLKAMGNRPNEMMDREKAYIPELQISFMEHIANPIYKL 873

; PRIOR FILING DATE: 2000-03-29
; PRIOR APPLICATION NUMBER: US 60/217,479
; PRIOR FILING DATE: 2000-07-11
; PRIOR APPLICATION NUMBER: US 60/221,014
; PRIOR FILING DATE: 2000-07-27
; Remaining Prior Application data removed - See File Wrapper or PALM.
; NUMBER OF SEQ ID NOS: 20
; SOFTWARE: PatentIn version 3.2
; SEQ ID NO 5
; LENGTH: 941
; TYPE: PRT
; ORGANISM: Homo Sapiens
US-10-686-282-5

Query Match          93.6%; Score 4474.5; DB 17; Length 941;
Best Local Similarity 94.7%; Pred. No. 0;
Matches 860; Conservative 21; Mismatches 26; Indels 1; Gaps 1;

QY 854 LQDLFPKAAELYERVASNRHWTKVSHKFTIRGLPNNNSLDPLDEBYEVPDLQCARAPIN 913
DB 874 LQDLFPKAAELYERVASNRHWTKVSHKFTIRGLPNNNSLDPLDEBYEVPDLQCARAPIN 933
QY 914 GCCLSDAE 921
DB 934 GCCLSDAE 941

RESULT 11
US-10-686-282-5
; Sequence 5, Application US/10686282
; Publication No. US20050020547A1
; GENERAL INFORMATION:
; APPLICANT: Pfizer Inc.
; APPLICANT: Maw, Graham Nigel
; APPLICANT: Wayman, Christopher Peter
; TITLE OF INVENTION: Compounds for the Treatment of Female Sexual Dysfunction
; FILE REFERENCE: PC10343D
; CURRENT APPLICATION NUMBER: US/10/686,282
; CURRENT FILING DATE: 2003-10-15
; PRIOR APPLICATION NUMBER: US 09/708,392
; PRIOR FILING DATE: 2000-11-08
; PRIOR APPLICATION NUMBER: US 60/175,161
; PRIOR FILING DATE: 2000-03-29
; PRIOR APPLICATION NUMBER: GB 9926437.6
; PRIOR FILING DATE: 1999-11-08
; PRIOR APPLICATION NUMBER: GB 0004021.2
; PRIOR FILING DATE: 2000-02-18
; PRIOR APPLICATION NUMBER: GB 0013001.3
; PRIOR FILING DATE: 2000-05-26
; PRIOR APPLICATION NUMBER: GB 0016563.9
; PRIOR FILING DATE: 2000-07-05
; PRIOR APPLICATION NUMBER: GB 0017141.3
; PRIOR FILING DATE: 2000-07-12
; PRIOR APPLICATION NUMBER: US 60/192,962
; PRIOR FILING DATE: 2000-03-29
; PRIOR APPLICATION NUMBER: US 60/217,479
; PRIOR FILING DATE: 2000-07-11
; PRIOR APPLICATION NUMBER: US 60/221,014
; PRIOR FILING DATE: 2000-07-27
; Remaining Prior Application data removed - See File Wrapper or PALM.
; NUMBER OF SEQ ID NOS: 20
; SOFTWARE: PatentIn version 3.2
; SEQ ID NO 5
; LENGTH: 941
; TYPE: PRT
; ORGANISM: Homo Sapiens
US-10-686-282-5

Query Match          93.6%; Score 4474.5; DB 17; Length 941;
Best Local Similarity 94.7%; Pred. No. 0;
Matches 860; Conservative 21; Mismatches 26; Indels 1; Gaps 1;

QY 14 QBPVPPGSGDALQDALLSLGSDVIDVAGLQQAQVKEALSAVLPKVTYTYLLDGSRLVC 73
DB 35 EPPPPQPCADSLQDALLSLGSDVIDISGLQRAVKEALSAVLPKVTYTYLLDGSRLVC 94
QY 74 EPPHLPQEGKREAVISRKRLGCGNGLGFSPLPGKPLARLVAPLAPDTQVLPVLDKE 133
DB 95 EPPHLPQEGKREAVISRKRLGCGNGLGFSPLPGKPLARLVAPLAPDTQVLPVLDKE 154
QY 134 AGAAVAVILVHCGQLSDNEEWSLQAVKHTLVALKRVQALQOQRESSVAPEATQNPPEAA 193
DB 155 AGAAVAVILVHCGQLSDNEEWSLQAVKHTLVALKRVQALQOQRESSVAPEATQNPPEAA 214
QY 194 GQKGGVATNDRKILQICGELYDLDASSLQKVLQYLQOQTRASRCCLLLVSEDLQL 253
DB 215 EDQKGGAAVTRDRKILQICGELYDLDASSLQKVLQYLQOQTRASRCCLLLVSEDLQL 274
QY 254 SKCVIGDKVLEBEISPLTTRGRLQGVVEDKKSITQLKDLTSEDQQQLQSMGCEVQAMLCV 313
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Db 275 SKVIGDKVLGEVSPFL-TGCLGVVEDKKSQIQKDLTSEDVQQLQSMGLCEQLQMLCV 333
Qy 314 PVISRATDQVVALACAFNKLGGDLFTDQDEHVIQHCFTYTSVLTSTLAFQKEQKLKCEC 373
Db 334 PVISRATDQVVALACAFNKLGGDLFTDQDEHVIQHCFTYTSVLTSTLAFQKEQKLKCEC 393
Qy 374 QALLQVAKNLFTHLDDVSVLLQEIITEARNLSNABICSVFLLDQNELVAKVDFDGVVDE 433
Db 394 QALLQVAKNLFTHLDDVSVLLQEIITEARNLSNABICSVFLLDQNELVAKVDFDGVVDE 453
Qy 434 SYEIRIPADQGIAGHVATTGQILNIPDAYAHPFLFYRGVDDSTGFRTRNLCFFIKENOE 493
Db 454 SYEIRIPADQGIAGHVATTGQILNIPDAYAHPFLFYRGVDDSTGFRTRNLCFFIKENOE 513
Qy 494 VIGVAELVNKINGPWFSKFDEDLATAFSIYCGISIAHSLLYKKVNEAQYRSHLANEMMY 553
Db 514 VIGVAELVNKINGPWFSKFDEDLATAFSIYCGISIAHSLLYKKVNEAQYRSHLANEMMY 573
Qy 554 HKVYSDDEYTKLLHDGIQPVAAIDSNFASFTYTPRSLPEDDTSMAILSMLQDMNFINNYK 613
Db 574 HKVYSDDEYTKLLHDGIQPVAAIDSNFASFTYTPRSLPEDDTSMAILSMLQDMNFINNYK 633
Qy 614 IDCPTLARFCFLMWKGYRDPYPHNMMHAFSVSHFCYLLYKNLELTNYLEDMEIFALFISC 673
Db 634 IDCPTLARFCFLMWKGYRDPYPHNMMHAFSVSHFCYLLYKNLELTNYLEDMEIFALFISC 693
Qy 674 MCHDLDRHGTNNNSFOVASKSVLAALYSSEGVSVMERHHPAQAIALNTHGNCNIFDHFSCRK 733
Db 694 MCHDLDRHGTNNNSFOVASKSVLAALYSSEGVSVMERHHPAQAIALNTHGNCNIFDHFSCRK 753
Qy 734 YQMLDLMRDIIILATDLAHLRIFKDLQKMAEYGVDRNKKOHHSLLLCLLMTSCDLSQOT 793
Db 754 YQMLDLMRDIIILATDLAHLRIFKDLQKMAEYGVDRNKKOHHSLLLCLLMTSCDLSQOT 813
Qy 794 KGWTKTRKIAELIYKEFFSQDLEKAMGNRPWEMMDREKAVIPELOISFMEHIAPIYKL 853
Db 814 KGWTKTRKIAELIYKEFFSQDLEKAMGNRPWEMMDREKAVIPELOISFMEHIAPIYKL 873
Qy 854 LODLFPKAAELYERVASNRHWTKVSHKFTIRGLPSNNSLDFLDEEYVDPDLGAPIN 913
Db 874 LODLFPKAAELYERVASNRHWTKVSHKFTIRGLPSNNSLDFLDEEYVDPDLGAPIN 933
Qy 914 GCCSLDAE 921
Db 934 GCCSLDAE 941
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## RESULT 12

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US-10-686-349-5
; Sequence 5, Application US/10686349
; Publication No. US20050070499A1
; GENERAL INFORMATION:
; APPLICANT: Pfizer Inc.
; APPLICANT: Pfizer Limited
; APPLICANT: Maw, Graham Nigel
; APPLICANT: Wayman, Christopher Peter
; TITLE OF INVENTION: Compounds for the Treatment of Female Sexual Dysfunction
; FILE REFERENCE: PC10343C
; CURRENT APPLICATION NUMBER: US/10/686,349
; CURRENT FILING DATE: 2003-10-15
; PRIOR APPLICATION NUMBER: US 09/708,392
; PRIOR FILING DATE: 2000-11-08
; PRIOR APPLICATION NUMBER: US 60/175,161
; PRIOR FILING DATE: 2000-03-29
; PRIOR APPLICATION NUMBER: GB 9926437.6
; PRIOR FILING DATE: 1999-11-08
; PRIOR APPLICATION NUMBER: GB 0004021.2
; PRIOR FILING DATE: 2000-02-18
; PRIOR APPLICATION NUMBER: GB 0013001.3
; PRIOR FILING DATE: 2000-05-26
; PRIOR APPLICATION NUMBER: GB 0016563.9
; PRIOR FILING DATE: 2000-07-05
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; PRIOR APPLICATION NUMBER: GB 0017141.3
; PRIOR FILING DATE: 2000-07-12
; PRIOR APPLICATION NUMBER: US 60/192,962
; PRIOR FILING DATE: 2000-03-29
; PRIOR APPLICATION NUMBER: US 60/217,479
; PRIOR FILING DATE: 2000-07-11
; PRIOR APPLICATION NUMBER: US 60/221,014
; PRIOR FILING DATE: 2000-07-27
; Remaining Prior Application data removed - See File Wrapper or PALM.
; NUMBER OF SEQ ID NOS: 20
; SOFTWARE: PatentIn version 3.2
; SEQ ID NO 5
; LENGTH: 941
; TYPE: PRT
; ORGANISM: Homo Sapiens
US-10-686-349-5
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Query Match 93.6%; Score 4474.5; DB 17; Length 941;
Best Local Similarity 94.7%; Pred. No. 0;
Matches 860; Conservative 21; Mismatches 26; Indels 1; Gaps 1;
Qy 14 QEPVPPGSGDALQDALLSLGSDIVAGLQQAQVKEALSAVLPKVETVYTYLLDGSRLVC 73
Db 35 EPPPPPPQPCADSLQDALLSLGSDIVAGLQQAQVKEALSAVLPKVETVYTYLLDGSRLVC 94
Qy 74 EEPHELPOEGKVPREAVISRKLCNGLGSPDLPGKPLARLVAPLADPTQVLPVLDKE 133
Db 95 EDPHELPOEGKVPREAVISRKLCNGLGSPDLPGKPLARLVAPLADPTQVLPVLDKE 154
Qy 134 AGAVAAVILVHCGQLSNEEWSLQAVEKHTI VALKRVQALQOQRESSVAPATQNPPEAA 193
Db 155 AGAVAAVILVHCGQLSNEEWSLQAVEKHTI VALKRVQALQOQRESSVAPATQNPPEAA 214
Qy 194 GDQKGVAYTNQDRKILQLCGELYDLDASSLQLKVLQVLYQOETQASRCLLLVSEDNLQL 253
Db 215 EDQKGGAAAYTDRDRKILQLCGELYDLDASSLQLKVLQVLYQOETQASRCLLLVSEDNLQL 274
Qy 254 SKVIGDKVLGEVSPFL-TGCLGVVEDKKSQIQKDLTSEDVQQLQSMGLCEQLQMLCV 313
Db 275 SKVIGDKVLGEVSPFL-TGCLGVVEDKKSQIQKDLTSEDVQQLQSMGLCEQLQMLCV 333
Qy 314 PVISRATDQVVALACAFNKLGGDLFTDQDEHVIQHCFTYTSVLTSTLAFQKEQKLKCEC 373
Db 334 PVISRATDQVVALACAFNKLGGDLFTDQDEHVIQHCFTYTSVLTSTLAFQKEQKLKCEC 393
Qy 374 QALLQVAKNLFTHLDDVSVLLQEIITEARNLSNABICSVFLLDQNELVAKVDFDGVVDE 433
Db 394 QALLQVAKNLFTHLDDVSVLLQEIITEARNLSNABICSVFLLDQNELVAKVDFDGVVDE 453
Qy 434 SYEIRIPADQGIAGHVATTGQILNIPDAYAHPFLFYRGVDDSTGFRTRNLCFFIKENOE 493
Db 454 SYEIRIPADQGIAGHVATTGQILNIPDAYAHPFLFYRGVDDSTGFRTRNLCFFIKENOE 513
Qy 494 VIGVAELVNKINGPWFSKFDEDLATAFSIYCGISIAHSLLYKKVNEAQYRSHLANEMMY 553
Db 514 VIGVAELVNKINGPWFSKFDEDLATAFSIYCGISIAHSLLYKKVNEAQYRSHLANEMMY 573
Qy 554 HKVYSDDEYTKLLHDGIQPVAAIDSNFASFTYTPRSLPEDDTSMAILSMLQDMNFINNYK 613
Db 574 HKVYSDDEYTKLLHDGIQPVAAIDSNFASFTYTPRSLPEDDTSMAILSMLQDMNFINNYK 633
Qy 614 IDCPTLARFCFLMWKGYRDPYPHNMMHAFSVSHFCYLLYKNLELTNYLEDMEIFALFISC 673
Db 634 IDCPTLARFCFLMWKGYRDPYPHNMMHAFSVSHFCYLLYKNLELTNYLEDMEIFALFISC 693
Qy 674 MCHDLDRHGTNNNSFOVASKSVLAALYSSEGVSVMERHHPAQAIALNTHGNCNIFDHFSCRK 733
Db 694 MCHDLDRHGTNNNSFOVASKSVLAALYSSEGVSVMERHHPAQAIALNTHGNCNIFDHFSCRK 753
Qy 734 YQMLDLMRDIIILATDLAHLRIFKDLQKMAEYGVDRNKKOHHSLLLCLLMTSCDLSQOT 793
Db 754 YQMLDLMRDIIILATDLAHLRIFKDLQKMAEYGVDRNKKOHHSLLLCLLMTSCDLSQOT 813
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QY 794 KGWKTRKIAELIYKEFFSQGDLKAMGNRPMMMDREKAYIPLOISFMEHIAMPIYKL 853
DB 814 KGWKTRKIAELIYKEFFSQGDLKAMGNRPMMMDREKAYIPLOISFMEHIAMPIYKL 873
QY 854 LQDLPPKAAELYERVASNRHWTKVSHKFTIRGLPSNNSLDPLDEEYVDPDLDGARAPIN 913
DB 874 LQDLPPKAAELYERVASNRHWTKVSHKFTIRGLPSNNSLDPLDEEYVDPDLDGTAPIN 933
QY 914 GCCSLDAE 921
DB 934 GCCSLDAE 941

RESULT 13
US-10-094-989-4
; Sequence 4, Application US/10094989
; Publication No. US20020115179A1
; GENERAL INFORMATION:
; APPLICANT: Wei, Ming-Hui et al
; TITLE OF INVENTION: ISOLATED HUMAN PHOSPHODIESTERASE
; TITLE OF INVENTION: PROTEINS, NUCLEIC ACID MOLECULES ENCODING HUMAN
; TITLE OF INVENTION: PHOSPHODIESTERASE PROTEINS, AND USES THEREOF
; FILE REFERENCE: CL001063DIV
; CURRENT APPLICATION NUMBER: US/10/094,989
; CURRENT FILING DATE: 2002-03-12
; PRIOR APPLICATION NUMBER: 09/754,250
; NUMBER OF SEQ ID NOS: 5
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 4
; LENGTH: 905
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-094-989-4

Query Match 93.6%; Score 4473.5; DB 13; Length 905;
Best Local Similarity 94.9%; Pred. No. 0;
Matches 860; Conservative 20; Mismatches 25; Indels 1; Gaps 1;

QY 16 PVPPGSGDGLQDALLSLGSDVIDAGLQAVKEALSAVLPKVTYTYLLDGSRLVCE 75
DB 1 PPPPQPCADSLQDALLSLGSDVIDISGLQAVKEALSAVLPKVTYTYLLDGSRLVCE 60
QY 76 PPHELPEQGVKREAVISRKRKLCNGLGPSDLPKGLARLAVAPLADPTQVLVPLVDKAG 135
DB 61 PPHELPEQGVKREAVISRKRKLCNGLGPSDLPKGLARLAVAPLADPTQVLVPLVDKAG 120
QY 136 AVAAVILVHCGQLSDNEEWSLQAVEKHTLVALKRVQALQOQRESSVAPENATQNPPEAAGD 195
DB 121 AVAAVILVHCGQLSDNEEWSLQAVEKHTLVALKRVQALQOQRESSVAPENATQNPPEAAGD 180
QY 196 QKGGVAYTNODRKILQLCGELYDLDAASSIQLKVLQYLOQETQASRCCLLLVSEDNQLQSC 255
DB 181 QKGGAAVYTDNRKILQLCGELYDLDAASSIQLKVLQYLOQETQASRCCLLLVSEDNQLQSC 240
QY 256 KVIGDKVLEEEISFPLTTGRLGQVVEDKKSIIQLKDLTSEDQMQLQSMGLGCEYQAMLCVPV 315
DB 241 KVIGDKVLEEVSPFL-TGCLQGVVEDKKSIIQLKDLTSEDVQQLQSMGLGCEYQAMLCVPV 299
QY 316 ISRTAQVVALACAFNKLGGDLFTDQDEHVIQHCFTYTSVLTSTLAFQKQKLCCEQA 375
DB 300 ISRTAQVVALACAFNKLGGDLFTDQDEHVIQHCFTYTSVLTSTLAFQKQKLCCEQA 359
QY 376 LLOVAKNLFTHLDDVSVLQELIITEARNLSNAEICSVPFLDQNELVAKVFDGCVVEDSEY 435
DB 360 LLOVAKNLFTHLDDVSVLQELIITEARNLSNAEICSVPFLDQNELVAKVFDGCVVEDSEY 419
QY 436 EIRIPADQGIAGHVATTGQILNIPAYAHPLFYRGVDDSTGFRTRNILLCFPIKKNQEVY 495
DB 420 EIRIPADQGIAGHVATTGQILNIPAYAHPLFYRGVDDSTGFRTRNILLCFPIKKNQEVY 479
QY 496 GVAELVNKINGPWFSPKFDLATAFSIYCGISIAHSLLYKKVNEAQYRSHLANEMMMYHM 555
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DB 480 GVAELVNKINGPWFSPKFDLATAFSIYCGISIAHSLLYKKVNEAQYRSHLANEMMMYHM 539
QY 556 KVSDEYTKLLHDGIQPVAAIDSNFASFTYTPRSLPEDDTSMALLSMLQDMNFNNYKID 615
DB 540 KVSDEYTKLLHDGIQPVAAIDSNFASFTYTPRSLPEDDTSMALLSMLQDMNFNNYKID 599
QY 616 CPTLARFCLMWKGGYRDPYHNHMAFSVSHFCYLLYKQLELTNYLEDMEIIPALFISCMC 675
DB 600 CPTLARFCLMWKGGYRDPYHNHMAFSVSHFCYLLYKQLELTNYLEDIEIPALFISCMC 659
QY 676 HDLDRGTNNNSFOVASKSVLAALYSSEGSVMRHHFAQAIAILNTHGCGNIFOHFSRKYQ 735
DB 660 HDLDRGTNNNSFOVASKSVLAALYSSEGSVMRHHFAQAIAILNTHGCGNIFOHFSRKYQ 719
QY 736 RMLDLMRDIIILATDLAHLRIKDLQKMAEVGYDRTNKHSHLLCLLMTSCDLSQTKG 795
DB 720 RMLDLMRDIIILATDLAHLRIKDLQKMAEVGYDRTNKHSHLLCLLMTSCDLSQTKG 779
QY 796 WKTTRKIAELIYKEFFSQGDLKAMGNRPMMMDREKAYIPLOISFMEHIAMPIYKLQ 855
DB 780 WKTTRKIAELIYKEFFSQGDLKAMGNRPMMMDREKAYIPLOISFMEHIAMPIYKLQ 839
QY 856 DLFPKAAELYERVASNRHWTKVSHKFTIRGLPSNNSLDPLDEEYVDPDLDGARAPINGC 915
DB 840 DLFPKAAELYERVASNRHWTKVSHKFTIRGLPSNNSLDPLDEEYVDPDLDGTAPINGC 899
QY 916 CSLDAE 921
DB 900 CSLDAE 905

RESULT 14
US-10-108-260A-2928
; Sequence 2928, Application US/10108260A
; Publication No. US20040005560A1
; GENERAL INFORMATION:
; APPLICANT: HELIX RESEARCH INSTITUTE
; TITLE OF INVENTION: NO. US20040005560A1el full length cDNA
; FILE REFERENCE: H1-A0106
; CURRENT APPLICATION NUMBER: US/10/108,260A
; CURRENT FILING DATE: 2002-03-27
; NUMBER OF SEQ ID NOS: 5458
; SOFTWARE: Patentin Ver. 2.1
; SEQ ID NO 2928
; LENGTH: 950
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-108-260A-2928

Query Match 86.8%; Score 4148.5; DB 15; Length 950;
Best Local Similarity 94.3%; Pred. No. 0;
Matches 800; Conservative 21; Mismatches 26; Indels 1; Gaps 1;

QY 14 QEPVPPGSGDGLQDALLSLGSDVIDAGLQAVKEALSAVLPKVTYTYLLDGSRLVCE 73
DB 104 EPPPPQPCADSLQDALLSLGSDVIDISGLQAVKEALSAVLPKVTYTYLLDGSRLVCE 163
QY 74 BEPPHELPEQGVKREAVISRKRKLCNGLGPSDLPKGLARLAVAPLADPTQVLVPLVDKX 133
DB 164 EDPPELPEQGVKREAVISRKRKLCNGLGPSDLPKGLARLAVAPLADPTQVLVPLVDKX 223
QY 134 AGAAVAVILVHCGQLSDNEEWSLQAVEKHTLVALKRVQALQOQRESSVAPENATQNPPEAA 193
DB 224 AGAAVAVILVHCGQLSDNEEWSLQAVEKHTLVALKRVQALQOQRESSVAPENATQNPPEAA 283
QY 194 GDQKGGVAYTNODRKILQLCGELYDLDAASSIQLKVLQYLOQETQASRCCLLLVSEDNQL 253
DB 284 EDQKGGAAVYTDNRKILQLCGELYDLDAASSIQLKVLQYLOQETQASRCCLLLVSEDNQL 343
QY 254 SKCVIGDKVLEEEISFPLTTGRLGQVVEDKKSIIQLKDLTSEDQMQLQSMGLGCEYQAMLCV 313
DB 344 SKCVIGDKVLEEVSPFL-TGCLQGVVEDKKSIIQLKDLTSEDVQQLQSMGLGCEYQAMLCV 402
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Qy 314 PVISRATQVVALACAFNKLGGDLFTDDEHVIOHCFTYVTLSTLAFQKQKCEC 373  
 Db 403 PVISRATQVVALACAFNKLGGDLFTDDEHVIOHCFTYVTLSTLAFQKQKCEC 462  
 Qy 374 QALLQVAKNLFTHLDDVSVLLQEIITEARNLSNAEICSVFLLDQNELVAKVFDGGVDE 433  
 Db 463 QALLQVAKNLFTHLDDVSVLLQEIITEARNLSNAEICSVFLLDQNELVAKVFDGGVDE 522  
 Qy 434 SYEIRIPADQIAGHVATTGQILNTPDAYAHPFLYRGVDDSTGFRNLCFPKKNQOE 493  
 Db 523 SYEIRIPADQIAGHVATTGQILNTPDAYAHPFLYRGVDDSTGFRNLCFPKKNQOE 582  
 Qy 494 VIGVAELVNKINGPWFSDDELATAFASYICGISTAHSLLYKKVNEAOYRSHLANEMMY 553  
 Db 593 VIGVAELVNKINGPWFSDDELATAFASYICGISTAHSLLYKKVNEAOYRSHLANEMMY 642  
 Qy 554 HMKVSDDEYTKLLHDGIQPVAAIDSNFASFTYTPRSLPEDDTSMAILSMLQDMNFINNYK 613  
 Db 643 HMKVSDDEYTKLLHDGIQPVAAIDSNFASFTYTPRSLPEDDTSMAILSMLQDMNFINNYK 702  
 Qy 614 IDCPTLAFCLMVKKGYPDPYHNNMHAFSVSHFCYLLYKNLELNYLEDMEIPALFISC 673  
 Db 703 IDCPTLAFCLMVKKGYPDPYHNNMHAFSVSHFCYLLYKNLELNYLEDIEIFALFISC 762  
 Qy 674 MCHLDHRTGNNNSFOVASKSVLAALYSSEGSVMERHHPAQATAILNTHGNCNIFDHF SRKD 733  
 Db 763 MCHLDHRTGNNNSFOVASKSVLAALYSSEGSVMERHHPAQATAILNTHGNCNIFDHF SRKD 822  
 Qy 734 YQRMDLMDRIILATDLAHLRIIPKDLQMAEVGYDRTNKQHHSLLLCLLMTSCDLSQOT 793  
 Db 823 YQRMDLMDRIILATDLAHLRIIPKDLQMAEVGYDRTNKQHHSLLLCLLMTSCDLSQOT 882  
 Qy 794 KGWTKTRKIAELIYKEFFSQGDLKAMGNRPWEMMDREKAYIPELQISFMEHIAPIYKL 853  
 Db 883 KGWTKTRKIAELIYKEFFSQGDLKAMGNRPWEMMDREKAYIPELQISFMEHIAPIYKL 942  
 Qy 854 LQDLFPKA 861  
 Db 943 LQDLFPKA 950

RESULT 15

US-10-104-047-2944  
 ; Sequence 2944, Application US/10104047  
 ; Publication No. US20030236392A1  
 ; GENERAL INFORMATION:  
 ; APPLICANT: HELIX RESEARCH INSTITUTE  
 ; TITLE OF INVENTION: NO. US20030236392A1el full length cdna  
 ; FILE REFERENCE: H1-A0105  
 ; CURRENT APPLICATION NUMBER: US/10/104,047  
 ; PRIOR FILING DATE: 2002-03-25  
 ; PRIOR APPLICATION NUMBER:  
 ; PRIOR FILING DATE:  
 ; NUMBER OF SEQ ID NOS: 4096  
 ; SOFTWARE: PatentIn Ver. 2.1  
 ; SEQ ID NO 2944  
 ; LENGTH: 786  
 ; TYPE: PRT  
 ; ORGANISM: Homo sapiens  
 US-10-104-047-2944

Query Match 74.1%; Score 3543.5; DB 15; Length 786;  
 Best Local Similarity 93.8%; Pred. No. 5.1e-289;  
 Matches 684; Conservative 21; Mismatches 23; Indels 1; Gaps 1;  
 Qy 1 MRROPAAASRDLPAGEPVPFGSDGALQDALLSLGSDVIDVAGLQQAQKALSAVLPKVETV 60  
 Db 1 MRROPAAASLDPLAKEPFGPSRDEDEALLSLGSDVIDISGLQRAVKEALSVAVLPRVETV 60  
 Qy 61 YTYLLDGSRLVCEBPPHELPOEGKVRBAVTSRKRLGNCGLGSPDLPKPLARLVAPLAP 120  
 Db 61 YTYLLDGSRLVCEBPPHELPOEGKVRBAVTSRKRLGNCGLGSPDLPKPLARLVAPLAP 120

Qy 121 DTQVLVPLVDKEAGAAVAVILVHCQGLSDNEEMSLQAVEKHTLVALKRVQALQORESSV 180  
 Db 121 DTQVLVPLVDKEAGAAVAVILVHCQGLSDNEEMSLQAVEKHTLVALKRVQALQOGRPRE 180  
 Qy 181 APEATQNPPEEAAGDQKGVATYTNQDRKILQCCGELYDLDDASSLQKLVLYLQETOASR 240  
 Db 181 APRAVQNPPECTAEDQKGAAYTDRDKILQCCGELYDLDDASSLQKLVLYLQETOASR 240  
 Qy 241 CCLLVSDNQLQCKVIGDKVLEBEISFPPLTQRLGQVVEDKKSIOQLKDLTSEBQOQLQ 300  
 Db 241 CCLLVSDNQLQCKVIGDKVLEBEISFPPLTQRLGQVVEDKKSIOQLKDLTSEBQOQLQ 299  
 Qy 301 SMLCEVQAMLCVPIVSRATQVVALACAFNKLGGDLFTDDEHVIOHCFTYVTLST 360  
 Db 300 SMLCEVQAMLCVPIVSRATQVVALACAFNKLGGDLFTDDEHVIOHCFTYVTLST 359  
 Qy 361 LAFQKEQKLCCEQALLQVAKNLFTHLDDVSVLLQEIITEARNLSNAEICSVFLLDQNEL 420  
 Db 360 LAFQKEQKLCCEQALLQVAKNLFTHLDDVSVLLQEIITEARNLSNAEICSVFLLDQNEL 419  
 Qy 421 VAKVFDGQVDESEYEIRIPADQIAGHVATTGQILNTPDAYAHPFLYRGVDDSTGFRTR 480  
 Db 420 VAKVFDGQVDESEYEIRIPADQIAGHVATTGQILNTPDAYAHPFLYRGVDDSTGFRTR 479  
 Qy 481 NILCFPIKNENQEVIGVAELVNKINGPWFSDDELATAFASYICGISTAHSLLYKKVNEA 540  
 Db 480 NILCFPIKNENQEVIGVAELVNKINGPWFSDDELATAFASYICGISTAHSLLYKKVNEA 539  
 Qy 541 QYRSHLANEMMYHMKVSDDEYTKLLHDGIQPVAAIDSNFASFTYTPRSLPEDDTSMAIL 600  
 Db 540 QYRSHLANEMMYHMKVSDDEYTKLLHDGIQPVAAIDSNFASFTYTPRSLPEDDTSMAIL 599  
 Qy 601 SMLQDMNFINNYKIDCPTLAFCLMVKKGYPDPYHNNMHAFSVSHFCYLLYKNLELNY 660  
 Db 600 SMLQDMNFINNYKIDCPTLAFCLMVKKGYPDPYHNNMHAFSVSHFCYLLYKNLELNY 659  
 Qy 661 LEDMEIFALFISCMCHDLDRGTNNNSFOVASKSVLAALYSSEGSVMERHHPAQATAILNT 720  
 Db 660 LEDMEIFALFISCMCHDLDRGTNNNSFOVASKSVLAALYSSEGSVMERHHPAQATAILNT 719  
 Qy 721 HGCNIFDHF 729  
 Db 720 HGCNIFDHF 728

Search completed: June 26, 2005, 12:40:58  
 Job time : 118.692 secs

GenCore version 5.1.6  
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OM protein - protein search, using sw model

Run on: June 26, 2005, 12:06:11 ; Search time 115.187 Seconds  
(without alignments)  
3092.423 Million cell updates/sec

Title: US-10-697-894-39  
Perfect score: 4781  
Sequence: 1 MRQPAASDLFAQEPVPG.....VPDLGARAPINGCCSLDAE 921

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 2105692 seqs, 386760381 residues

Total number of hits satisfying chosen parameters: 2105692

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database : A\_Geneseq\_16Dec04:\*

1: Geneseq1980s:\*

2: Geneseq1990s:\*

3: Geneseq2000s:\*

4: Geneseq2001s:\*

5: Geneseq2002s:\*

6: Geneseq2003s:\*

7: Geneseq2003bs:\*

8: Geneseq2004s:\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

## SUMMARIES

Result No.	Score	Match	Length	DB ID	Description
1	4781	100.0	921	2 AAR69727	AAR69727 Cyclic-GM
2	4781	100.0	921	2 AAW11252	AAW11252 Clone p3C
3	4781	100.0	921	2 AAW18048	AAW18048 Cyclic-GM
4	4781	100.0	921	2 AAW71224	AAW71224 CGS-PDE e
5	4781	100.0	921	2 AAW77040	AAW77040 Adrenal c
6	4781	100.0	921	2 AAW60752	AAW60752 CGS-PDE i
7	4781	100.0	921	3 AAY80984	AAY80984 Bovine ad
8	4781	100.0	921	6 ABUS8723	ABUS8723 Bovine ad
9	4781	100.0	921	8 ADQ94959	ADQ94959 Bovine p3
10	4764	99.6	921	2 AAR28407	AAR28407 CGS-PDE f
11	4657	97.4	942	2 AAR69728	AAR69728 Cyclic-GM
12	4657	97.4	942	2 AAW11239	AAW11239 Cyclic GM
13	4657	97.4	942	2 AAW18049	AAW18049 CGS-PDE a
14	4657	97.4	942	2 AAW71225	AAW71225 Bovine br
15	4657	97.4	942	2 AAW77041	AAW77041 Cyclic-GM
16	4657	97.4	942	2 AAW60753	AAW60753 CGS-PDE i
17	4657	97.4	942	3 AAY80985	AAY80985 Bovine br
18	4657	97.4	942	3 ABUS8724	ABUS8724 Bovine br
19	4657	97.4	942	8 ADQ94963	ADQ94963 Bovine CG
20	4617	96.6	942	2 AAR28408	AAR28408 CGS PDE f
21	4539.5	94.9	920	6 ABR54205	ABR54205 Human NOV
22	4533.5	94.8	920	5 AAO15507	AAO15507 Human NOV
23	4533.5	94.8	920	5 AAG70998	AAG70998 Human pho
24	4474.5	93.6	941	2 AAR69729	AAR69729 Cyclic-GM
25	4474.5	93.6	941	2 AAW11253	AAW11253 pHCgs6n c

## ALIGNMENTS

## RESULT 1

AAR69727

ID AAR69727 standard; protein; 921 AA.

AC AAR69727;

XX

XX

DT 25-MAR-2003 (revised)

DT 11-OCT-1995 (first entry)

XX

DE Cyclic-GMP stimulated nucleotide PDE clone p3CGS-5.

XX

KW Cyclic-GMP stimulated nucleotide phospho-diesterase; antibodies;

KW bovine adrenal cortex; hormones; neurotransmitters;

KW transmission regulation; enzyme purification; clone p3CGS-5.

XX

OS Bos taurus.

XX

PN US5389527-A.

XX

PD 14-FEB-1995.

XX

PF 20-APR-1992; 92US-00872644.

XX

PR 19-APR-1991; 91US-00688356.

XX

PA (UNIW ) UNIV WASHINGTON.

XX

PI Sonnenburg WK, Charbonneau H, Beavo JA;

XX

WPI; 1995-090205/12.

XX

DR N-PSDB; AAQ83974.

XX

PT New nucleic acid encoding cyclic-GMP stimulated nucleotide phospho-

PT diesterase - and related vectors and transformed cells, useful for

XX screening cpds. for phospho-di:esterase modulating activity.

XX

PS Claim 1; Col 65-74; 69pp; English.

XX

CC AAQ83974 encodes AAR69727 the bovine adrenal cortex cyclic-GMP stimulated

CC nucleotide phospho-diesterase (Cam PDE) clone p3CGS-5. Eukaryotic cells

CC that express Cam PDE can be used to screen cpds. for the ability to

CC modulate Cam PDE activity. Cam PDEs are involved in regulating the

CC transmission of information from hormones, neurotransmitters or other

CC systems that use cyclic nucleotides as messengers. Antibodies raised

CC against Cam PDE can be used for enzyme purificn., or determination.

XX (Updated on 25-MAR-2003 to correct PF field.)

XX Sequence 921 AA;

26 4474.5 93.6 941 2 AAW18050 Aaw18050 Human CGS  
27 4474.5 93.6 941 2 AAW71226 Aaw71226 Human CGS  
28 4474.5 93.6 941 2 AAW77042 Aaw77042 Cyclic-GM  
29 4474.5 93.6 941 2 AAW60754 Aaw60754 Human CGS  
30 4474.5 93.6 941 3 AAY80986 Aay80986 Human CGS  
31 4474.5 93.6 941 4 AAS07954 Aae07954 Human pho  
32 4474.5 93.6 941 4 AAS07918 Aae07918 Human pho  
33 4474.5 93.6 941 4 AAB85117 Aab85117 Human CGM  
34 4474.5 93.6 941 4 AAB85106 Aab85106 Human CGM  
35 4474.5 93.6 941 4 AAG66539 Aag66539 Human int  
36 4474.5 93.6 941 6 ABUS8725 Abus8725 Human bra  
37 4474.5 93.6 941 7 ADD14154 Add14154 Human bra  
38 4474.5 93.6 941 7 ADE62314 Ade62314 Human pro  
39 4474.5 93.6 941 8 ADO21792 Ado21792 Human pho  
40 4474.5 93.6 941 8 ADQ94965 Adq94965 Plasmid p  
41 4436.5 92.8 941 2 AAR28409 Aar28409 Human foe  
42 4324.5 90.5 928 7 ADE62312 Ade62312 Rat Prote  
43 4148.5 86.8 950 7 ADM04243 Adm04243 Human pro  
44 3543.5 74.1 786 7 ADB64790 Adb64790 Human pro  
45 3229 67.5 685 8 ADR10446 ADR10446 Human pro

```
Query Match      100.0%; Score 4781; DB 2; Length 921;
Best Local Similarity 100.0%; Pred. No. 0;
Matches 921; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 MRRQPAASRDLPFAQEPVPPGSDGALQDALLSLGSDVIDVAGLQQAQVKEALSAPLKVETV 60
DB 1 MRRQPAASRDLPFAQEPVPPGSDGALQDALLSLGSDVIDVAGLQQAQVKEALSAPLKVETV 60
QY 61 YTYLLDGSRLVCEPPEPHELPOEGKREAVISRKLGCNGLGPSDLPGKPLARLVAIPLAP 120
DB 61 YTYLLDGSRLVCEPPEPHELPOEGKREAVISRKLGCNGLGPSDLPGKPLARLVAIPLAP 120
QY 121 DTQVLVPLVDKEAGAAVAAILVHCGQLSDNEEWSLQAVEKHTLVALKRVQALQORESSV 180
DB 121 DTQVLVPLVDKEAGAAVAAILVHCGQLSDNEEWSLQAVEKHTLVALKRVQALQORESSV 180
QY 181 APEATQNPPEEAAGQKGGVAYTNQDRKILQICGELYDLDASSLQKVLQVYLQOQTQASR 240
DB 181 APEATQNPPEEAAGQKGGVAYTNQDRKILQICGELYDLDASSLQKVLQVYLQOQTQASR 240
QY 241 CCLLVSDNLSQSKVIGDKVLEBEISFPPLTTGRLGVVEDKKGSIQKDLTSEDMDQQLQ 300
DB 241 CCLLVSDNLSQSKVIGDKVLEBEISFPPLTTGRLGVVEDKKGSIQKDLTSEDMDQQLQ 300
QY 301 SMLGCEVQAMLCVPIVRATDOVVALACAFNKLGGDLFTDQDEHVIQCFHYTSTVLST 360
DB 301 SMLGCEVQAMLCVPIVRATDOVVALACAFNKLGGDLFTDQDEHVIQCFHYTSTVLST 360
QY 361 LAFQKEQKLKCEQALLQVAKNLFTHLDDVSVLLQEIITEARNLSNABICSVFLDDQNEL 420
DB 361 LAFQKEQKLKCEQALLQVAKNLFTHLDDVSVLLQEIITEARNLSNABICSVFLDDQNEL 420
QY 421 VAKVPDGGVDESEYIIRIPADQGIAGHVATTGQILNIPDAYAHPLFYRGVDDSDTGFTR 480
DB 421 VAKVPDGGVDESEYIIRIPADQGIAGHVATTGQILNIPDAYAHPLFYRGVDDSDTGFTR 480
QY 481 NILCPPIKNEQVIGVLAELVKNKNGPWSKFEDELFATFSTYCGISIAHSLLYKKVNEA 540
DB 481 NILCPPIKNEQVIGVLAELVKNKNGPWSKFEDELFATFSTYCGISIAHSLLYKKVNEA 540
QY 541 QYRSHLANEMMYHMKVSDDEYTKLLHDGIQPVAIDSNFASFTYTPRSLPEDDTSMAL 600
DB 541 QYRSHLANEMMYHMKVSDDEYTKLLHDGIQPVAIDSNFASFTYTPRSLPEDDTSMAL 600
QY 601 SMLQDMFNINNYKIDCPTLARFCLMVKKGYRDPYPHNNMHAFSVSHFCYLLYKNLELTY 660
DB 601 SMLQDMFNINNYKIDCPTLARFCLMVKKGYRDPYPHNNMHAFSVSHFCYLLYKNLELTY 660
QY 661 LEDMEIFALFTSCMCHDLDRGTNNNSFQVASKSVLAALYSSEGSVNERHHFAQATAILNT 720
DB 661 LEDMEIFALFTSCMCHDLDRGTNNNSFQVASKSVLAALYSSEGSVNERHHFAQATAILNT 720
QY 721 HGCNIFDHFSRKDYQRMOLDLMDRIILATDLAHLRIFKDLQMAEVGYDRTNKQHSLLL 780
DB 721 HGCNIFDHFSRKDYQRMOLDLMDRIILATDLAHLRIFKDLQMAEVGYDRTNKQHSLLL 780
QY 781 CLLMTSCDLSQDTKGWTKTRKIAELIYKEFFSQGDLKAMGNRPMMMDREKAYIPELQI 840
DB 781 CLLMTSCDLSQDTKGWTKTRKIAELIYKEFFSQGDLKAMGNRPMMMDREKAYIPELQI 840
QY 841 SFMEHIANPIYKLLQDLFPKAAELYERVAENREHWTKVSHKFTIRGLPSNNSLDPLDEY 900
DB 841 SFMEHIANPIYKLLQDLFPKAAELYERVAENREHWTKVSHKFTIRGLPSNNSLDPLDEY 900
QY 901 EVPDLGAPINGCCSLDAE 921
DB 901 EVPDLGAPINGCCSLDAE 921
```

RESULT 2  
AAW11252

ID AAW11252 standard; protein; 921 AA.

```
XX AC AAW11252;
XX 25-MAR-2003 (revised)
XX 17-MAR-1997 (first entry)
XX Clone p3CGS-5 cyclic GMP stimulated phosphodiesterase.
XX Cyclic GMP stimulated phosphodiesterase; cGS-PDE; bovine; brain; cAMP;
XX adrenal gland; cGMP; transmembrane signal; extracellular hormone;
XX neurotransmitter; antibody.
XX Bos taurus.
XX US5580771-A.
XX 03-DEC-1996.
XX 29-AUG-1994; 94US-00297494.
XX 19-APR-1991; 91US-00688356.
XX 20-APR-1992; 92US-00872644.
XX (UNIW ) UNIV WASHINGTON.
XX Charbonneau H, Sonnenburg WK, Beavo JA;
XX WPI; 1997-033573/03.
XX N-PSDB; AAT51110.
XX DNA encoding cGMP-stimulated phosphodiesterase - for prodn. of
XX recombinant enzyme.
XX Example 4; Col 65-72; 68pp; English.
XX This sequence represents the cyclic GMP stimulated phosphodiesterase (cGS
XX -PDE) clone p3CGS-5 isolated from bovine adrenal cortex. The cyclic
XX nucleotide phosphodiesterases (PDEs) catalyze the hydrolysis of 3', 5'
XX cyclic nucleotides, such as cAMP and cGMP, to their corresponding 5'
XX nucleotide monophosphates. The PDEs are therefore important in the
XX control of the cellular concentration of cyclic nucleotides. The PDEs
XX are, in turn, regulated by transmembrane signals or second messenger
XX ligands such as calcium ion or cGMP. The PDEs therefore have a central
XX role in regulating the flow of information from extracellular hormones,
XX neurotransmitters, or other signals that use the cyclic nucleotides as
XX messengers. PDEs are present in most of the cells and tissues of
XX eukaryotic organisms, but only in trace amounts. cGS-PDEs are stimulated
XX by cGMP in effecting cAMP hydrolysis. This is thought to occur through a
XX noncatalytic cGMP-specific site present on the cGS-PDE. The cDNA encoding
XX this sequence can be used for the production of recombinant cGS-PDE.
XX which may have therapeutic and diagnostic uses. This protein may also be
XX useful for diagnostic antibody production. (Updated on 25-MAR-2003 to
XX correct PF field.)
```

Sequence 921 AA;

Query Match 100.0%; Score 4781; DB 2; Length 921;
Best Local Similarity 100.0%; Pred. No. 0;
Matches 921; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

```
QY 1 MRRQPAASRDLPFAQEPVPPGSDGALQDALLSLGSDVIDVAGLQQAQVKEALSAPLKVETV 60
DB 1 MRRQPAASRDLPFAQEPVPPGSDGALQDALLSLGSDVIDVAGLQQAQVKEALSAPLKVETV 60
QY 61 YTYLLDGSRLVCEPPEPHELPOEGKREAVISRKLGCNGLGPSDLPGKPLARLVAIPLAP 120
DB 61 YTYLLDGSRLVCEPPEPHELPOEGKREAVISRKLGCNGLGPSDLPGKPLARLVAIPLAP 120
QY 121 DTQVLVPLVDKEAGAAVAAILVHCGQLSDNEEWSLQAVEKHTLVALKRVQALQORESSV 180
DB 121 DTQVLVPLVDKEAGAAVAAILVHCGQLSDNEEWSLQAVEKHTLVALKRVQALQORESSV 180
QY 181 APEATQNPPEEAAGQKGGVAYTNQDRKILQICGELYDLDASSLQKVLQVYLQOQTQASR 240
```



```

Db      181  APEATQNPPEAAGDQGGVAYTNQDRKILQCGELYDLDASSLQKVLQYQQETQASR 240
Qy      241  CCLLLVSEDNLQLSCKVIGDKVLEEBEISFPLTTGRGLGQVVEDEKKSITQLKDLTSEDMMQQLQ 300
Db      241  CCLLLVSEDNLQLSCKVIGDKVLEEBEISFPLTTGRGLGQVVEDEKKSITQLKDLTSEDMMQQLQ 300
Qy      301  SMLGCEVQAMLCVPVISRATDQVVALACAFNKLGGDLFTDQDEHVIQHCFTSTVLTST 360
Db      301  SMLGCEVQAMLCVPVISRATDQVVALACAFNKLGGDLFTDQDEHVIQHCFTSTVLTST 360
Qy      361  LAFQEKQKLKCECOALLQVAKNLFTHLDDVSVLLQEIITEARNLSNAEICSVFLLDQNEL 420
Db      361  LAFQEKQKLKCECOALLQVAKNLFTHLDDVSVLLQEIITEARNLSNAEICSVFLLDQNEL 420
Qy      421  VAKVFDGGVVEDESEYIRIPADQGIAGHVATTGQILNIPDAYAHPLFYRGVDDSTGFRTR 480
Db      421  VAKVFDGGVVEDESEYIRIPADQGIAGHVATTGQILNIPDAYAHPLFYRGVDDSTGFRTR 480
Qy      481  NILCFPIKNEQVEIGVAELVKNKINGPWFSKFDEDLATAFSIYCGISIAHSLLYKKNVNEA 540
Db      481  NILCFPIKNEQVEIGVAELVKNKINGPWFSKFDEDLATAFSIYCGISIAHSLLYKKNVNEA 540
Qy      541  QYRSHLANEMMYHMKVSDDEYTKLLHDGIQPVAAIDSNFASFTYTPRSLPEDDTSMAIL 600
Db      541  QYRSHLANEMMYHMKVSDDEYTKLLHDGIQPVAAIDSNFASFTYTPRSLPEDDTSMAIL 600
Qy      601  SMLQDMNFNNYKIDCPTLARCLMVKKGYRPPYHNMWHAFSVSHFCYLLYNLELNTY 660
Db      601  SMLQDMNFNNYKIDCPTLARCLMVKKGYRPPYHNMWHAFSVSHFCYLLYNLELNTY 660
Qy      661  LEDMEIFALFISCMCHDLDRGTNNSFQVASKSVLAALYSSEGSVMERHHPAQAIILNT 720
Db      661  LEDMEIFALFISCMCHDLDRGTNNSFQVASKSVLAALYSSEGSVMERHHPAQAIILNT 720
Qy      721  HCCNIPDFHSRKYORMLDLARDIILATDLAHLRIFKDLQMAEVGYDRTNKQHSLLL 780
Db      721  HCCNIPDFHSRKYORMLDLARDIILATDLAHLRIFKDLQMAEVGYDRTNKQHSLLL 780
Qy      781  CLLMTSCDLSQDTGKWKTRKIAELIYKEFFSQGDLKAMGNRPMEMMDREKAYIPELQI 840
Db      781  CLLMTSCDLSQDTGKWKTRKIAELIYKEFFSQGDLKAMGNRPMEMMDREKAYIPELQI 840
Qy      841  SPMEHIAMPIYKLLQDLPPKAAELYERVASNREHWTKVSHKFTIRGLFSPNNSLDFLDEY 900
Db      841  SPMEHIAMPIYKLLQDLPPKAAELYERVASNREHWTKVSHKFTIRGLFSPNNSLDFLDEY 900
Qy      901  EYVDLDGARAPINGCCSLDAE 921
Db      901  EYVDLDGARAPINGCCSLDAE 921

```

```

RESULT 3
AAW18048
ID  AAW18048 standard; protein; 921 AA.
XX
AC  AAW18048;
XX
DT  25-MAR-2003 (revised)
DT  05-AUG-1997 (first entry)
XX
DE  Cyclic-GMP-stimulated phosphodiesterase (cGS-PDE) from p3CGS-5.
XX
KW  Ca2+/calmodulin stimulated cyclic nucleotide phosphodiesterase enzyme;
KW  calcium ion; antibody; cow; polymerase chain reaction.
XX
OS  Bos taurus.
XX
PN  US5602019-A.
XX
PD  11-FEB-1997.
XX
PP  29-AUG-1994; 94US-00297510.

```

```

XX      19-APR-1991; 91US-00688356.
PR      20-APR-1992; 92US-00872644.
XX
PA      (UNIW ) UNIV WASHINGTON.
XX
PI      Sonnenburg WK, Charbonneau H, Bentley JK, Beavo JA;
XX
DR      WPI; 1997-131799/12.
DR      N-PSDB; AAT67220.
XX
PT      DNA encoding bovine and human phosphodiesterase enzymes - stimulated by
PT      calcium/calmodulin, useful for recombinant prodn. of the enzymes.
XX
PS      Example 4; Col 73-78; 69pp; English.
XX
CC      The present sequence represents the amino acid sequence from the large
CC      open reading frame of p3CGS-5 cDNA bovine adrenal cortex clone insert.
CC      The presence of 36 adenosine residues at the 3'-end of the cDNA preceded
CC      by a transcription termination consensus sequence suggests that all of
CC      the 3' untranslated sequence of the cyclic-GMP-stimulated
CC      phosphodiesterase (cGS-PDE) mRNA is represented by this clone. The DNA
CC      sequences of the cGS-PDE's are used for the production of the recombinant
CC      enzymes, which in turn may be used for antibody production and to screen
CC      for compounds that modulate phosphodiesterase activity. (Updated on 25-
CC      MAR-2003 to correct PF field.) (Updated on 25-MAR-2003 to correct PI
CC      field.)
XX
SQ      Sequence 921 AA;
XX
Query Match 100.0%; Score 4781; DB 2; Length 921;
Best Local Similarity 100.0%; Pred. No. 0;
Matches 921; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
Qy      1  MRPPAASRDILFAQEPVPPGSGDGLQDALLSLGSLVIVAGLQQAQKALSAPLKVETV 60
Db      1  MRPPAASRDILFAQEPVPPGSGDGLQDALLSLGSLVIVAGLQQAQKALSAPLKVETV 60
Qy      61  YTYLLDGSRLVCEBPPELPOEGKVRNAVTSRKELGNGLGPSDLPGKPLARLVAFLAP 120
Db      61  YTYLLDGSRLVCEBPPELPOEGKVRNAVTSRKELGNGLGPSDLPGKPLARLVAFLAP 120
Qy      121  DTQVLVPLVDKEAGAAVAVILVHCGQLSDNEWSLQAVEKHTLVALKRVQALQRESSV 180
Db      121  DTQVLVPLVDKEAGAAVAVILVHCGQLSDNEWSLQAVEKHTLVALKRVQALQRESSV 180
Qy      181  APEATQNPPEAAGDQGGVAYTNQDRKILQCGELYDLDASSLQKVLQYQQETQASR 240
Db      181  APEATQNPPEAAGDQGGVAYTNQDRKILQCGELYDLDASSLQKVLQYQQETQASR 240
Qy      241  CCLLLVSEDNLQLSCKVIGDKVLEEBEISFPLTTGRGLGQVVEDEKKSITQLKDLTSEDMMQQLQ 300
Db      241  CCLLLVSEDNLQLSCKVIGDKVLEEBEISFPLTTGRGLGQVVEDEKKSITQLKDLTSEDMMQQLQ 300
Qy      301  SMLGCEVQAMLCVPVISRATDQVVALACAFNKLGGDLFTDQDEHVIQHCFTSTVLTST 360
Db      301  SMLGCEVQAMLCVPVISRATDQVVALACAFNKLGGDLFTDQDEHVIQHCFTSTVLTST 360
Qy      361  LAFQEKQKLKCECOALLQVAKNLFTHLDDVSVLLQEIITEARNLSNAEICSVFLLDQNEL 420
Db      361  LAFQEKQKLKCECOALLQVAKNLFTHLDDVSVLLQEIITEARNLSNAEICSVFLLDQNEL 420
Qy      421  VAKVFDGGVVEDESEYIRIPADQGIAGHVATTGQILNIPDAYAHPLFYRGVDDSTGFRTR 480
Db      421  VAKVFDGGVVEDESEYIRIPADQGIAGHVATTGQILNIPDAYAHPLFYRGVDDSTGFRTR 480
Qy      481  NILCFPIKNEQVEIGVAELVKNKINGPWFSKFDEDLATAFSIYCGISIAHSLLYKKNVNEA 540
Db      481  NILCFPIKNEQVEIGVAELVKNKINGPWFSKFDEDLATAFSIYCGISIAHSLLYKKNVNEA 540
Qy      541  QYRSHLANEMMYHMKVSDDEYTKLLHDGIQPVAAIDSNFASFTYTPRSLPEDDTSMAIL 600
Db      541  QYRSHLANEMMYHMKVSDDEYTKLLHDGIQPVAAIDSNFASFTYTPRSLPEDDTSMAIL 600

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Qy	601	SMLQDMFNINNYKIDCPTLARFCLMVKKGYRDPDPYHNWMAFVSVSHFCVLLYKNULELNTY	660
Db	601	SMLQDMFNINNYKIDCPTLARFCLMVKKGYRDPDPYHNWMAFVSVSHFCVLLYKNULELNTY	660
Qy	661	LEDMEIFALFISCMCHDLDHRTGNNNSFOVASKSVLAALYSSEGSVMERHHFAQAI TALNT	720
Db	661	LEDMEIFALFISCMCHDLDHRTGNNNSFOVASKSVLAALYSSEGSVMERHHFAQAI TALNT	720
Qy	721	HGCNIFDHFSSKDYQVMDLMDRIIATDLAHLRI FKDLQKAEVGVDRDTNKQHSLLL	780
Db	721	HGCNIFDHFSSKDYQVMDLMDRIIATDLAHLRI FKDLQKAEVGVDRDTNKQHSLLL	780
Qy	781	CLLMTSCDLSQDTKGWTKTRKIAELIYKEFFSQGDLKAMGNRPNEMMDREKAYIPELQI	840
Db	781	CLLMTSCDLSQDTKGWTKTRKIAELIYKEFFSQGDLKAMGNRPNEMMDREKAYIPELQI	840
Qy	841	SFMEHIAMPIYKLLQDLFPKAAELYERVASNREHWTKVSHKFTIRGLPSNNSLDFLDEEY	900
Db	841	SFMEHIAMPIYKLLQDLFPKAAELYERVASNREHWTKVSHKFTIRGLPSNNSLDFLDEEY	900
Qy	901	EVPLD GARAPINGCCSLDAE	921
Db	901	EVPLD GARAPINGCCSLDAE	921

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## RESULTS

AAW/1224

ID AAW71224

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AC AAW71224;

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29-OCT-19

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through pathways involving these, regulate flow of information from extracellular hormones, neurotransmitters and other signals using cyclic nucleotides as messengers. The specification describes an assay for identifying a chemical agent which modifies the enzymatic activity of a mammalian CaM-PDE. The assays are useful for identifying modulators of CaM-PDEs. The assay is carried out by incubating cells expressing CaM-PDE with the suspected modulator and measuring its effect e.g. monitoring the hydrolysis of cAMP and/or cGMP

Sequence 921 AA:

**Cinema Match**

100 04 - Cinema 4781 - DD 3 - Tenth 021.

Query Match

Best Local Similarity 100.0%; Pred. No. 0;

Qy	1	MRRQPAASRDLFAQEPVP	PGSGDGLAQDALLSLG	SVTDVAGLQAVKEALSAVLPKVETV	60		
Db	1	MRRQPAASRDLFAQEPVP	PGSGDGLAQDALLSLG	SVTDVAGLQAVKEALSAVLPKVETV	60		
Qy	61	YTYLLDGESRLVCEEP	HELPOBQKVREAVTSR	KRLGCGNGIPGSDLPCKPLARLVAPLAP	120		
Db	61	YTYLLDGESRLVCEEP	HELPOBQKVREAVTSR	KRLGCGNGIPGSDLPCKPLARLVAPLAP	120		
Qy	121	DTQVLVIPLVDKEAGA	VAAVILVHCGQLSDNE	EWLSQAVEKHTLVALKRVQALQORESSV	180		
Db	121	DTQVLVIPLVDKEAGA	VAAVILVHCGQLSDNE	EWLSQAVEKHTLVALKRVQALQORESSV	180		
Qy	181	APBATOQNPPEAAGDQ	KGVAAYTNDRKIIQL	CGELYDLASSLQLVQLVLOOETOQASR	240		
Db	181	APBATOQNPPEAAGDQ	KGVAAYTNDRKIIQL	CGELYDLASSLQLVQLVLOOETOQASR	240		
Qy	241	CCLLLVSEDLQJLSC	KVIGDKVLEEBISFP	LTTRGLGOVVEDKKSIQLKJLTSDDMOQLQ	300		
Db	241	CCLLLVSEDLQJLSC	KVIGDKVLEEBISFP	LTTRGLGOVVEDKKSIQLKJLTSDDMOQLQ	300		
Qy	301	SMLGCEVQAMLCVP	VISRATDQVVALACA	FNKLGSDLFTDQDEHVIQHC	FHYTSTVL	360	
Db	301	SMLGCEVQAMLCVP	VISRATDQVVALACA	FNKLGSDLFTDQDEHVIQHC	FHYTSTVL	360	
Qy	361	LAFQKEOKLKCEQAL	LQVAKNLFTHLDDV	SVLLQEIITEARNLSNABICSV	FLDDQNEL	420	
Db	361	LAFQKEOKLKCEQAL	LQVAKNLFTHLDDV	SVLLQEIITEARNLSNABICSV	FLDDQNEL	420	
Qy	421	VAKVFDGGVVEDS	YEIRIPADOGIAGH	VAATTGQILNIPDAYAHLFVRG	VDDSTGPRTR	480	
Db	421	VAKVFDGGVVEDS	YEIRIPADOGIAGH	VAATTGQILNIPDAYAHLFVRG	VDDSTGPRTR	480	
Qy	481	NILCFPIKNEQVIG	VAELVNKINGPWF	SKFDEDLATAFSIYCGISIAH	SLLYKKVNEA	540	
Db	481	NILCFPIKNEQVIG	VAELVNKINGPWF	SKFDEDLATAFSIYCGISIAH	SLLYKKVNEA	540	
Qy	541	QYRSHLANEMMM	THMKVSDDEYTKL	HDGQTPVAAIDSNFASFTYTPR	SLPEDDTSMAIL	600	
Db	541	QYRSHLANEMMM	THMKVSDDEYTKL	HDGQTPVAAIDSNFASFTYTPR	SLPEDDTSMAIL	600	
Qy	601	SMLOQMNFINNY	KIDCPTLARFCILM	VKKGYRDPYPHNWMAFVS	YSHFCYLLYKNLEL	660	
Db	601	SMLOQMNFINNY	KIDCPTLARFCILM	VKKGYRDPYPHNWMAFVS	YSHFCYLLYKNLEL	660	
Qy	661	LEDMEIFALPIS	CMWCHDLHRGTN	NSFQVAKSVLAALYSEGS	VMERHHPAQAI	720	
Db	661	LEDMEIFALPIS	CMWCHDLHRGTN	NSFQVAKSVLAALYSEGS	VMERHHPAQAI	720	
Qy	721	HGCNIFDHF	SRKDYQRMJLMD	RIILATDLAH	LURI FKDLQKMAE	VGDRTNKQHSLLL	780
Db	721	HGCNIFDHF	SRKDYQRMJLMD	RIILATDLAH	LURI FKDLQKMAE	VGDRTNKQHSLLL	780
Qy	781	CLLMTSCDLS	DQTKGWTKTKIAE	LIYKEFPF	SQGDLEKAMGNR	PWEMMDREKAYIPELOI	840
Db	781	CLLMTSCDLS	DQTKGWTKTKIAE	LIYKEFPF	SQGDLEKAMGNR	PWEMMDREKAYIPELOI	840
Qy	841	SFMEHIAMPYI	KLQDLFPKAAEL	YERVASNREH	WTKVSHKPTTRIG	LPSSNNSLDFLDBEY	900

Db	841	SPMEHAPIYKLLQDLFPKAAELYERVASNRHHTKVKSHKFTIRGLPSNNSLDFLDESY	900
Qy	901	EVPDLGAPINGCCSLDAE	921
Db	901	EVPDLGAPINGCCSLDAE	921
RESULT 5			
AAW77040	ID	AAW77040 standard; protein; 921 AA.	
XX	AC	AAW77040;	
XX	DT	09-NOV-1998 (first entry)	
XX	DE	Adrenal cortex Ca2+/calmodulin stimulated phosphodiesterase.	
XX	ss;	cow; Ca2+ stimulated phosphodiesterase;	
KW	KW	Calmodulin stimulated phosphodiesterase; therapeutic; antibody.	
XX	Bos sp.		
XX	OS	US5789553-A.	
XX	PN	04-AUG-1998.	
XX	PD	31-MAY-1995; 95US-00455526.	
XX	PF	19-APR-1991; 91US-00698356.	
XX	PR	20-APR-1992; 92US-00872644.	
XX	PR	29-AUG-1994; 94US-00297494.	
XX	PA	(UNIW ) UNIV WASHINGTON.	
XX	PI	Sonnenburg WK, Charbonneau H, Beavo JA, Bentley JK;	
XX	DR	WPI; 1998-446185/38.	
XX	DR	N-PSDB; AAV48201.	
XX	PT	Antibody to phosphodiesterase polypeptide - useful for purification or	
XX	PT	detection of polypeptide.	
XX	PS	Example 4; Col 65-72; 68pp; English.	
XX	CC	The adrenal cortex Ca2+/calmodulin stimulated phosphodiesterase is one of	
XX	CC	several phosphodiesterases isolated in this invention, used to transform	
XX	CC	host cells, preferably mammalian or yeast cells. The recombinant proteins	
XX	CC	and fragments produced can be used for therapeutic, diagnostic, and	
XX	CC	prognostic purposes and will provide the basis for preparation of	
XX	CC	monoclonal and polyclonal antibodies. An antibody specific for the	
XX	CC	Ca2+/calmodulin-stimulated cyclic nucleotide phosphodiesterase (PDE)	
XX	CC	polypeptide is useful for affinity purification or detection of the	
XX	CC	polypeptide and is selective only for the Ca2+/calmodulin stimulated	
XX	CC	cyclic nucleotide PDE polypeptide	
XX	SQ	Sequence 921 AA;	
Query Match 100.0%; Score 4781; DB 2; Length 921;			
Best Local Similarity 100.0%; Pred. No. 0;			
Matches 921; Conservative 0; Mismatches 0; Indels 0; Gaps 0			
Qy	1	MRROPAAASRDLFAGEPVPVPGSGDGLQDALLSLGSSVIDVAGLQQAVKEALSAVLPKVTY	60
Db	1	MRROPAAASRDLFAGEPVPVPGSGDGLQDALLSLGSSVIDVAGLQQAVKEALSAVLPKVTY	60
Qy	61	YTYLLDGSRLVCEBPVPHLPQEGKVRBAVTSRKLRCNGLGPSDLPGKPLARLVAPLAP	120
Db	61	YTYLLDGSRLVCEBPVPHLPQEGKVRBAVTSRKLRCNGLGPSDLPGKPLARLVAPLAP	120
Qy	121	DTQVLVITPLVDKEAGAAVAVILVHCCQLSDNEEWSLQAVEKHTLVALKRVQALQORESSV	180
Db	121	DTQVLVITPLVDKEAGAAVAVILVHCCQLSDNEEWSLQAVEKHTLVALKRVQALQORESSV	180



PS	Claim 1; Col 71-76; 69pp; English.	
XX	The invention relates to purified and isolated nucleotide sequences encoding mammalian Ca <sup>2+</sup> /calmodulin-stimulated phosphodiesterases (Cam-PDEs) and cyclic guanine monophosphate (cGMP)-stimulated phosphodiesterases (cGS-PDEs). In particular the invention relates to an assay for identifying chemicals that modify the enzymatic activity of a mammalian cGS-PDE. The PDEs catalyze the hydrolysis of cyclic nucleotides to their corresponding 5'-nucleoside monophosphates. In this way they control the cellular concentration of cyclic nucleotides, thereby regulating the flow of information from extracellular hormones, neurotransmitters or other signals that use cyclic nucleotides as messengers. The PDEs in turn are regulated by transmembrane signals or second messenger ligands such as Ca <sup>2+</sup> or cGMP. Inhibitors of these enzymes are potentially useful as cardiotonics, antidepressants, antihypertensives or antithrombotics. The method of the invention can identify specific inhibitors of particular isoforms of cGS-PDEs. Sequences AAY80968, AAY80972, AAY80975, AAY80977, AAY80984-Y80986, and AAY80988-Y80990 represent isoforms of Cam-PDEs and cGS-PDEs from bovines and humans	
XX	Sequence 921 AA;	
SQ	Query Match 100.0%; Score 4781; DB 3; Length 921; Best Local Similarity 100.0%; Pred. No. 0; Matches 921; Conservative 0; Mismatches 0; Indels 0; Gaps 0;	
QY	1 MRQPAASRDLEPAQEPVPGSGDQALQDALLSGVSDVAGLQQAQVKEALSAPLKVETV 60	661 LEDMEIFALFISCMCHDLHRGTNNNSFQVASKSVLAALYSSEGSVMERHHFAQAIALNT 720
DB	1 MRQPAASRDLEPAQEPVPGSGDQALQDALLSGVSDVAGLQQAQVKEALSAPLKVETV 60	721 HGCNIFDHFPSRKYQRMQLDMRDIIILATDLAHLRIFKDLQKMAEYGYDRTNKQHSLLL 780
QY	61 YTYLLDGSRLVCEBPPELPOEGKVREAVISRKLGCGNLGSPDIPGKPLARLAPLAP 120	721 HGCNIFDHFPSRKYQRMQLDMRDIIILATDLAHLRIFKDLQKMAEYGYDRTNKQHSLLL 780
DB	61 YTYLLDGSRLVCEBPPELPOEGKVREAVISRKLGCGNLGSPDIPGKPLARLAPLAP 120	781 CLUMTSCDLSQDTQGWKTKRKAELIYKFFSQGDLEKAMGNRPMEMDREKAYIPELQI 840
QY	121 DTQVLVIPLVDEKAGNAVILVHCGQLSDNEWSLQAVEKHTLVALKRQVQLQRESSV 180	781 CLUMTSCDLSQDTQGWKTKRKAELIYKFFSQGDLEKAMGNRPMEMDREKAYIPELQI 840
DB	121 DTQVLVIPLVDEKAGNAVILVHCGQLSDNEWSLQAVEKHTLVALKRQVQLQRESSV 180	841 SPMEHIAPIYKLLQDLPPKAAELVERVASNREHWTKVSHKPTIRGLPSNNSLDFLDEEY 900
QY	181 APEATQNPPEAAGQKGVATYNDQRKILQCGELYDLQSSLQKVLQYLOQETQASR 240	841 SPMEHIAPIYKLLQDLPPKAAELVERVASNREHWTKVSHKPTIRGLPSNNSLDFLDEEY 900
DB	181 APEATQNPPEAAGQKGVATYNDQRKILQCGELYDLQSSLQKVLQYLOQETQASR 240	901 EYVPLDGGARAPINGCCSLDAE 921
QY	241 CCLLVSEDNLQSKVIGDKVLEBIEISPLTTGRIGQVVEDKSIQLKDLTSDMQQLQ 300	901 EYVPLDGGARAPINGCCSLDAE 921
DB	241 CCLLVSEDNLQSKVIGDKVLEBIEISPLTTGRIGQVVEDKSIQLKDLTSDMQQLQ 300	RESULT 8
QY	301 SMLGCEVQAMLCVPVISRATDQVVALACAFNKLGGDLFTDQDEHVIQHCFTYTVLST 360	ABUS8723
DB	301 SMLGCEVQAMLCVPVISRATDQVVALACAFNKLGGDLFTDQDEHVIQHCFTYTVLST 360	ID ABUS8723 standard; protein; 921 AA.
QY	361 LAFQKEQKLCQCOALLQVAKNLFTHLDVSVLLQELIITEARNLSNAEICSVPFLDDQNEL 420	XX AC ABUS8723;
DB	361 LAFQKEQKLCQCOALLQVAKNLFTHLDVSVLLQELIITEARNLSNAEICSVPFLDDQNEL 420	XX DT 15-APR-2003 (first entry)
QY	421 VAKVFDGGVDESEYIRIPADQGIAGHVATTGQILNIPDAYHPLFYRGVDDSTGFRT 480	XX DE Bovine adrenal cortex cGS-PDE.
DB	421 VAKVFDGGVDESEYIRIPADQGIAGHVATTGQILNIPDAYHPLFYRGVDDSTGFRT 480	XX KW Cow; Ca <sup>2+</sup> /calmodulin stimulated phosphodiesterase; enzyme; Cam-PDE; 59Kda Cam-PDE; 61Kda Cam-PDE; 63Kda Cam-PDE; cGS-PDE;
QY	481 NTLCPPIKNEQEVIGVABLNVKNGPWFPSKFEDEDLATAFSYICGISTAHSLLYKKVNEA 540	XX KW Cyclic GMP-stimulated phosphodiesterase; cardiotoxic agent; antidepressant; anti-hypertensive; anti-thrombotic.
DB	481 NTLCPPIKNEQEVIGVABLNVKNGPWFPSKFEDEDLATAFSYICGISTAHSLLYKKVNEA 540	XX OS Bos taurus.
QY	541 QYRSHLANEMMYHMKVSDEYTKLLHDGIQPVAIDSNFASFTYTPRSLPDDTSMALL 600	XX PN US2002151024-A1.
DB	541 QYRSHLANEMMYHMKVSDEYTKLLHDGIQPVAIDSNFASFTYTPRSLPDDTSMALL 600	XX PD 17-OCT-2002.
QY	601 SMLQDMNFNNYKIDCPTLARFCLMVKGYRPPYHNMWHAFSVSHFCVLLYKNELTNY 660	XX PF 18-JUN-2001; 2001US-00883825.
DB	601 SMLQDMNFNNYKIDCPTLARFCLMVKGYRPPYHNMWHAFSVSHFCVLLYKNELTNY 660	XX PR 19-APR-1991; 91US-00688356.
QY	661 LEDMEIFALFISCMCHDLHRGTNNNSFQVASKSVLAALYSSEGSVMERHHFAQAIALNT 720	XX PR 20-APR-1992; 92US-00872644.
		XX PR 31-MAY-1995; 95US-00455526.
		XX PR 28-JUL-1998; 98US-00123783.
		XX PA (UNITW ) UNIV WASHINGTON.
		XX PI Beavo JA, Bentley JK, Charbonneau H, Sonnenburg WK;
		XX DR WPI; 2003-198291/19.
		XX DR N-PSDB; ABX78854.
		XX PT New purified and isolated DNA sequence encoding a mammalian calcium/calmodulin- or cyclic GMP-stimulated cyclic nucleotide phosphodiesterase polypeptide, useful for therapeutic, diagnostic and prognostic applications.
		XX PS Example 4; Page 39-42; 71pp; English.
		XX CC The invention relates to purified and isolated polynucleotide sequence encoding a mammalian Ca <sup>2+</sup> /calmodulin- or cyclic GMP-stimulated cyclic nucleotide phosphodiesterase polypeptide (Cam-PDE and cGS-PDE). Also included are a DNA vector comprising the novel DNA sequence, a host cell transformed with the polynucleotide sequence, a polypeptide product of the expression in the transformed host cell, an antibody specifically immunoreactive with the polypeptide and assay methods for identifying a chemical agent which modifies the enzymatic activity of a mammalian Cam-PDE or cGS-PDE. Disclosed are the cDNA and protein sequences of bovine 59Kda Cam-PDE, 61Kda Cam-PDE, 63Kda Cam-PDE, cGS-PDE and human 61Kda Cam-PDE and cGS-PDE. The DNA sequence is useful for producing a polypeptide having the enzymatic activity of a mammalian Cam-PDE or cGS-PDE which is

CC used in therapeutic, diagnostic and prognostic applications and in the  
CC preparation of antibodies. Isolated chemical agents which are inhibitors  
CC of PDEs may have anti-depressant, anti- hypertensive or anti-thrombotic  
CC activities or may be cardiotoxic agents. The present sequence is a Bovine  
XX CaM-PDE or CGS-PDE (or fragment) of the invention  
SQ Sequence 921 AA;

Query Match 100.0%; Score 4781; DB 6; Length 921;  
Best Local Similarity 100.0%; Pred. No. 0;  
Matches 921; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 MRROPAAARDLFAQEPVPPGSGDGLQDALLSLGSLVIVAGLQAVKEALSAPLKVETV 60  
Db 1 MRROPAAARDLFAQEPVPPGSGDGLQDALLSLGSLVIVAGLQAVKEALSAPLKVETV 60  
Qy 61 YTYLLDGSRLVCEPPHPELQEGKVRBAVSRKELGNCGLGPSDLPGKPLARLVAPLAP 120  
Db 61 YTYLLDGSRLVCEPPHPELQEGKVRBAVSRKELGNCGLGPSDLPGKPLARLVAPLAP 120  
Qy 121 DTQVLVIFLVDEKAGAAVILVHCGQLSDNEEWSLQAVEKHTLVALKRVQALQORESSV 180  
Db 121 DTQVLVIFLVDEKAGAAVILVHCGQLSDNEEWSLQAVEKHTLVALKRVQALQORESSV 180  
Qy 181 APEATONPPEAAGDKGVAVTNODRKILQICGELYDLDASSLQQLKVLQYLQESTQASR 240  
Db 181 APEATONPPEAAGDKGVAVTNODRKILQICGELYDLDASSLQQLKVLQYLQESTQASR 240  
Qy 241 CCLLVSDNQLQSKVIGDKVLEBEISFPLTTGRLGQVVEDKKSQIKDLTSDMQQLQ 300  
Db 241 CCLLVSDNQLQSKVIGDKVLEBEISFPLTTGRLGQVVEDKKSQIKDLTSDMQQLQ 300  
Qy 301 SMLGCEVQAMLCVPVISRATQVVALACAFNKLGGDLFTDQDEHVIQCHFYTSTVLTST 360  
Db 301 SMLGCEVQAMLCVPVISRATQVVALACAFNKLGGDLFTDQDEHVIQCHFYTSTVLTST 360  
Qy 361 LAFQKEQKLKCEQALLQVAKNLFTHLDDVSVLLQEIITEARNLSNAEICSVFLLDQNEL 420  
Db 361 LAFQKEQKLKCEQALLQVAKNLFTHLDDVSVLLQEIITEARNLSNAEICSVFLLDQNEL 420  
Qy 421 VAKVFDGCVGVEDSEYIIRIPADQGIAGHVATTGQILNIPDAYAHPFLYRGVDDSTGFRT 480  
Db 421 VAKVFDGCVGVEDSEYIIRIPADQGIAGHVATTGQILNIPDAYAHPFLYRGVDDSTGFRT 480  
Qy 481 NILCFPIKNQEVIGVAVLNKNGPWFSPFDEDLATAFSIYCGISTAHSLLYKKNEA 540  
Db 481 NILCFPIKNQEVIGVAVLNKNGPWFSPFDEDLATAFSIYCGISTAHSLLYKKNEA 540  
Qy 541 QYRSHLANEMMYHMKVSDDEYTKLLHDGIIQPVAAIDSNPASFTVTPRSLPEDDTSMAIL 600  
Db 541 QYRSHLANEMMYHMKVSDDEYTKLLHDGIIQPVAAIDSNPASFTVTPRSLPEDDTSMAIL 600  
Qy 601 SMLQDMNFNNYKIDCPTLARFCLMVKKGYRDPDPYHNMWHAFSVSHFCYLLYKNLELTNY 660  
Db 601 SMLQDMNFNNYKIDCPTLARFCLMVKKGYRDPDPYHNMWHAFSVSHFCYLLYKNLELTNY 660  
Qy 661 LEDMEIFALFTSCMCHDLDRGTNNNSFOVASKSVLAALYSSEGSMERHHFAQIAIINT 720  
Db 661 LEDMEIFALFTSCMCHDLDRGTNNNSFOVASKSVLAALYSSEGSMERHHFAQIAIINT 720  
Qy 721 HGCNIFDHFSRKDYQRMULDARDIILATDLAHLRI PKDLQMAEVGYDRTNKQHLSLL 780  
Db 721 HGCNIFDHFSRKDYQRMULDARDIILATDLAHLRI PKDLQMAEVGYDRTNKQHLSLL 780  
Qy 781 CLLMTSCDLSQDTKGWKTTRKIAELIYKEFFSQGDLEKAMGNRPMEMMDREKAYIPELQI 840  
Db 781 CLLMTSCDLSQDTKGWKTTRKIAELIYKEFFSQGDLEKAMGNRPMEMMDREKAYIPELQI 840  
Qy 841 SFMEHIAMPIYKLLQDLFPKAAELYERVASNREHWTKVSHKFTTIRGLPSNNSLDFLDEEY 900  
Db 841 SFMEHIAMPIYKLLQDLFPKAAELYERVASNREHWTKVSHKFTTIRGLPSNNSLDFLDEEY 900  
Qy 901 EVPDLDGARAPINGCCSLDAE 921

Db 901 EVPDLDGARAPINGCCSLDAE 921  
RESULT 9  
ADQ94959  
ID ADQ94959 standard; protein; 921 AA.  
AC ADQ94959;  
XX 23-SEP-2004 (first entry)  
XX Bovine p3CGS-5 clone insert cDNA encoding protein.  
XX CaM-PDE;  
KW Ca 2+/ calmodulin stimulated cyclic nucleotide phosphodiesterase; cGMP;  
KW cyclic-guanosine monophosphate; cGS-PDE;  
KW cyclic-GMP stimulated cyclic nucleotide phosphodiesterase; bovine.  
XX Bos sp.  
OS US2004126866-A1.  
FN 01-JUL-2004.  
PD 30-OCT-2003; 2003US-00697894.  
PF 19-APR-1991; 91US-00688356.  
XX 20-APR-1992; 92US-00872644.  
PR 29-AUG-1994; 94US-00297494.  
PR 31-MAY-1995; 95US-00455526.  
PR 28-JUL-1998; 98US-00123783.  
PR 18-JUN-2001; 2001US-00883825.  
XX (BEAV/) BEAVO J A.  
PA (BENT/) BENTLEY J K.  
PA (CHAR/) CHARBONNEAU H.  
XX (SONN/) SONNENBURG W K.  
FI Beavo JA, Bentley JK, Charbonneau H, Sonnenburg WK;  
XX WPI; 2004-516912/49.  
DR N-PSDB; ADQ94958.  
XX Novel mammalian calcium/calmodulin stimulated cyclic phosphodiesterase  
PT nucleotide sequence useful for identifying chemical agent that modifies  
PT enzymatic activity of calcium/calmodulin stimulated cyclic  
PT phosphodiesterase polypeptide.  
XX Example 4; SEQ ID NO 39; 72pp; English.  
XX The present invention provides a mammalian Ca 2+/ calmodulin stimulated  
CC cyclic nucleotide phosphodiesterase (CaM-PDE) and cyclic-guanosine  
CC monophosphate (cGMP) stimulated cyclic nucleotide phosphodiesterase (CGS-  
CC PDE) polypeptide and its polynucleotide. The invention is useful for  
CC producing a polypeptide having enzymatic activity of mammalian CaM-PDE  
CC and CGS-PDE. The invention is also useful for identifying a chemical  
CC agent that modifies the enzymatic activity of mammalian CaM-PDE and CGS-  
CC PDE. The present sequence is bovine p3CGS-5 clone insert cDNA encoding  
CC protein.  
SQ Sequence 921 AA;

Query Match 100.0%; Score 4781; DB 8; Length 921;  
Best Local Similarity 100.0%; Pred. No. 0;  
Matches 921; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
Qy 1 MRROPAAARDLFAQEPVPPGSGDGLQDALLSLGSLVIVAGLQAVKEALSAPLKVETV 60  
Db 1 MRROPAAARDLFAQEPVPPGSGDGLQDALLSLGSLVIVAGLQAVKEALSAPLKVETV 60  
Qy 61 YTYLLDGSRLVCEPPHPELQEGKVRBAVSRKELGNCGLGPSDLPGKPLARLVAPLAP 120

Db 61 YTYLLDGSRLVCBPPHLPQEGKREAVISRKLGCGNGLSPDLPGKPLARLVAPLAP 120  
Qy 121 DTQVLVPLVDKEAGAAVAVILVHCCQLSDNEWSLQAVEKHTLVALKRVQALQORESSV 180  
Db 121 DTQVLVPLVDKEAGAAVAVILVHCCQLSDNEWSLQAVEKHTLVALKRVQALQORESSV 180  
Qy 181 APEATONPPEEAAGDQKGGVATNQDRKILQCGELYDLASSLQIKVLYLQOQTQASR 240  
Db 181 APEATONPPEEAAGDQKGGVATNQDRKILQCGELYDLASSLQIKVLYLQOQTQASR 240  
Qy 241 CCLLLVSEDNLQLSCKVIGDKVLEEEISFPLTTGRLGVVDEKSIQKDLTSEDMDQLQ 300  
Db 241 CCLLLVSEDNLQLSCKVIGDKVLEEEISFPLTTGRLGVVDEKSIQKDLTSEDMDQLQ 300  
Qy 301 SMLGCEVQAMLCVVISRATDQVVALACAFNKLGGDLFTDQDEHVIQHCFTYTVLST 360  
Db 301 SMLGCEVQAMLCVVISRATDQVVALACAFNKLGGDLFTDQDEHVIQHCFTYTVLST 360  
Qy 361 LAFQKEQKLKCECQALLQVAKNLFTHLDDVSVLLQEIITEARNLSNAEICSVFLLDQNEL 420  
Db 361 LAFQKEQKLKCECQALLQVAKNLFTHLDDVSVLLQEIITEARNLSNAEICSVFLLDQNEL 420  
Qy 421 VAKVFDGGVDESEYIIRIPADQGIAGHVATTGQILNIPDAYAHPLFVRGVDDSTGFRTR 480  
Db 421 VAKVFDGGVDESEYIIRIPADQGIAGHVATTGQILNIPDAYAHPLFVRGVDDSTGFRTR 480  
Qy 481 NILCFPIKNEQEVIGVAELVKNKINGPWFSPFDEDLATAFSIYCGISIAHSLLYKKNVNEA 540  
Db 481 NILCFPIKNEQEVIGVAELVKNKINGPWFSPFDEDLATAFSIYCGISIAHSLLYKKNVNEA 540  
Qy 541 QYRSHLANEMMYHMKVSDDEYTKLLHGGIQPVAIDSNFASFTYTPRSLPEDDTSMAIL 600  
Db 541 QYRSHLANEMMYHMKVSDDEYTKLLHGGIQPVAIDSNFASFTYTPRSLPEDDTSMAIL 600  
Qy 601 SMLQDMFNINNYKIDCPTLAFCLMVKGYRDPDPVHNMHAFSVSHFCYLLYKNLELTYN 660  
Db 601 SMLQDMFNINNYKIDCPTLAFCLMVKGYRDPDPVHNMHAFSVSHFCYLLYKNLELTYN 660  
Qy 661 LEDMEIFALFISCMCHDLDRGTNNSFOVASKSVLAALYSSEGSMVRRHFAQAIILNT 720  
Db 661 LEDMEIFALFISCMCHDLDRGTNNSFOVASKSVLAALYSSEGSMVRRHFAQAIILNT 720  
Qy 721 HGCNIFDHFSDKDYQRMLDLRDIIILATDLAHLRIFKDLQMAEVGYDRNTKQHSLLL 780  
Db 721 HGCNIFDHFSDKDYQRMLDLRDIIILATDLAHLRIFKDLQMAEVGYDRNTKQHSLLL 780  
Qy 781 CLMTSCDLSDOTKGWKTTRKIAELIYKEFFSQGDLEKAMGNRPMEMMDREKAYIPELOI 840  
Db 781 CLMTSCDLSDOTKGWKTTRKIAELIYKEFFSQGDLEKAMGNRPMEMMDREKAYIPELOI 840  
Qy 841 SFMEHIAMPIYKLLQDLFPKAAELYERVASNREHWTKVSHKFTIRGLPSNNSLDFLDEY 900  
Db 841 SFMEHIAMPIYKLLQDLFPKAAELYERVASNREHWTKVSHKFTIRGLPSNNSLDFLDEY 900  
Qy 901 EVPDLGAPINGCCSLDAE 921  
Db 901 EVPDLGAPINGCCSLDAE 921

## RESULT 10

AAR28407  
ID AAR28407 standard; protein; 921 AA.

XX AC AAR28407;

DT 25-MAR-2003 (revised)

DT 19-MAR-1993 (first entry)

XX CGS-PDE from clone 3CGS-5, from bovine adrenal cortex.

DE Cyclic GMP; stimulated; cyclic; nucleotide; phosphodiesterase.

XX Bos taurus.

OS

XX

FN WO9218541-A1.

XX 29-OCT-1992.

XX 20-APR-1992; 92WO-US0003222.

XX 19-APR-1991; 91US-00688356.

XX (UNIW ) UNIV WASHINGTON.

XX Beavo JA, Bentley JK, Charbonneau H, Sonnenburg WK;

XX WPI; 1992-382051/46.

XX N-PSDB; AAQ30180.

XX New DNA encoding mammalian cyclic nucleotide phospho-di-esterase - and derived vectors and host cells, useful for screening cpds. for inhibitory or activating activity.

XX Example 4; Page 83; 133pp; English.

XX An unamplified bovine adrenal cortex cDNA library was prepd. and screened with redundant 23-mer antisense oligonucleotide probes end labelled with radiolabelled ATP and T4 polynucleotide kinase. A single 2.1 kb cDNA clone (designated pcgs-3:2.1) was obt'd. This clone was used to screen a second, amplified bovine adrenal cortex cDNA library to yield 52 putative clones. The largest insert was of 4.2 kb in a plasmid designated p3CGS-5. The cDNA encodes a 921 residue protein with mol. wt. 103 kD. (Updated on 25-MAR-2003 to correct PN field.)

XX Sequence 921 AA;

Query Match 99.6%; Score 4764; DB 2; Length 921;

Best Local Similarity 99.7%; Pred. No. 0;

Matches 918; Conservative 2; Mismatches 1; Indels 0; Gaps 0;

Qy 1 MRRPAAASRDILFAQEPVPPGSGDQALQDALLSLGSDVIDVAGLQQAQVKEALSAVLPKVT 60

Db 1 MRRPAAASRDILFAQEPVPPGSGDQALQDALLSLGSDVIDVAGLQQAQVKEALSAVLPKVT 60

Qy 61 YTYLLDGSRLVCBPPHLPQEGKREAVISRKLGCGNGLSPDLPGKPLARLVAPLAP 120

Db 61 YTYLLDGSRLVCBPPHLPQEGKREAVISRKLGCGNGLSPDLPGKPLARLVAPLAP 120

Qy 121 DTQVLVPLVDKEAGAAVAVILVHCCQLSDNEWSLQAVEKHTLVALKRVQALQORESSV 180

Db 121 DTQVLVPLVDKEAGAAVAVILVHCCQLSDNEWSLQAVEKHTLVALKRVQALQORESSV 180

Qy 181 APEATONPPEEAAGDQKGGVATNQDRKILQCGELYDLASSLQIKVLYLQOQTQASR 240

Db 181 APEATONPPEEAAGDQKGGVATNQDRKILQCGELYDLASSLQIKVLYLQOQTQASR 240

Qy 241 CCLLLVSEDNLQLSCKVIGDKVLEEEISFPLTTGRLGVVDEKSIQKDLTSEDMDQLQ 300

Db 241 CCLLLVSEDNLQLSCKVIGDKVLEEEISFPLTTGRLGVVDEKSIQKDLTSEDMDQLQ 300

Qy 301 SMLGCEVQAMLCVVISRATDQVVALACAFNKLGGDLFTDQDEHVIQHCFTYTVLST 360

Db 301 SMLGCEVQAMLCVVISRATDQVVALACAFNKLGGDLFTDQDEHVIQHCFTYTVLST 360

Qy 361 LAFQKEQKLKCECQALLQVAKNLFTHLDDVSVLLQEIITEARNLSNAEICSVFLLDQNEL 420

Db 361 LAFQKEQKLKCECQALLQVAKNLFTHLDDVSVLLQEIITEARNLSNAEICSVFLLDQNEL 420

Qy 421 VAKVFDGGVDESEYIIRIPADQGIAGHVATTGQILNIPDAYAHPLFVRGVDDSTGFRTR 480

Db 421 VAKVFDGGVDESEYIIRIPADQGIAGHVATTGQILNIPDAYAHPLFVRGVDDSTGFRTR 480

Qy 481 NILCFPIKNEQEVIGVAELVKNKINGPWFSPFDEDLATAFSIYCGISIAHSLLYKKNVNEA 540

Db 481 NILCFPIKNEQEVIGVAELVKNKINGPWFSPFDEDLATAFSIYCGISIAHSLLYKKNVNEA 540











monophosphate-stimulated phosphodiesterase (cGS-PDE) cDNA. The					
specification also describes Ca2+/calmodulin sensitive cyclic nucleotide					
phosphodiesterase (Cam-PDE) enzymes. Cam-PDE enzymes catalyze the					
hydrolysis of cyclic nucleotides and as such control their intracellular					
level. They are controlled by second messengers e.g. Ca2+ and calmodulin					
and transmembrane signals and through pathways involving these, regulate					
flow of information from extracellular hormones, neurotransmitters and					
other signals using cyclic nucleotides as messengers. The specification					
describes an assay for identifying a chemical agent which modifies the					
enzymatic activity of a mammalian Cam-PDE. The assays are useful for					
identifying modulators of Cam-PDBs. The assay is carried out by					
incubating cells expressing Cam-PDB with the suspected modulator and					
measuring its effect e.g. monitoring the hydrolysis of cAMP and/or cGMP					
CC	SQ	Sequence 942 AA;			
		Query Match	97.4%;	Score 4657;	DB 2; Length 942;
		Best Local Similarity	98.9%;	Pred. No. 0;	
		Matches 898;	Conservative 3;	Mismatches 7;	Indels 0; Gaps 0;
QY	14	QEPVPPGGDGLADALLSLGSDVDAGLQAQVKEALSAVLPKVETVTYTYLLDGESRLVC	73		
DB	35	EPPPPPQCADSLQDALLSLGSDVDAGLQAQVKEALSVPKVETVTYTYLLDGESRLVC	94		
QY	74	EPPPELHPQEGKVEAEIVSRKRLCGNGLGPSDLPGKPLARLVAPLADPTQVLVIPLVDXK	133		
DB	95	EPPPELHPQEGKVEAEIVSRKRLCGNGLGPSDLPGKPLARLVAPLADPTQVLVIPLVDXE	154		
QY	134	AGAAVAAILVHCGQLSNEEWSLOAQEKHTVALVKRYONLQOORESSVAPEATQNPPRENA	193		
DB	155	AGAAVAAILVHCGQLSNEEWSLOAQEKHTVALVKRYOALQOORESSVAPEATQNPPBEA	214		
QY	194	GDQKGGVAYTDQRKIQLCGELYDLDASSIQLKLVLQYLQOETQASRCCLLLVSEDNLIQL	253		
DB	215	GDQKGGVAYTDQRKIQLCGELYDLDASSIQLKLVLQYLQOETQASRCCLLLVSEDNLIQL	274		
QY	254	SKCVIGDKVLEEBEISFFPLTTGRLGQVVEDKKSIQLKDLTSEDMMQOLSMLGCEVOAMLCV	313		
DB	275	SKCVIGDKVLEEBEISFFPLTTGRLGQVVEDKKSIQLKDLTSEDMMQOLSMLGCEVOAMLCV	334		
QY	314	PVTSRAFDQVVVALACAFNKLGGDLFTDDDEHVIOHCFTHYTSTVLTSITLAFQKEOKLKCEC	373		
DB	335	PVTSRAFDQVVVALACAFNKLGGDLFTDDDEHVIOHCFTHYTSTVLTSITLAFQKEOKLKCEC	394		
QY	374	QALLQVAKNLFTHLDDVSLLQEIIITEARNLSNAEICSVFLLDQNELVAKVDFGCVGEDE	433		
DB	395	QALLQVAKNLFTHLDDVSLLQEIIITEARNLSNAEICSVFLLDQNELVAKVDFGCVGEDE	454		
QY	434	SYEIRIPADGGIAGHVATTGQILNPDAYAHPLFYRGVDDSGTPRTNNILCFPIKNENQE	493		
DB	455	SYEIRIPADGGIAGHVATTGQILNPDAYAHPLFYRGVDDSGTPRTNNILCFPIKNENQE	514		
QY	494	VIGVAELVNKINGPWFSPKFDEDLATASIYCGISIAHSLLYKKVNEAQYSHLANEMMY	553		
DB	515	VIGVAELVNKINGPWFSPKFDEDLATASIYCGISIAHSLLYKKVNEAQYSHLANEMMY	574		
QY	554	HMKVSDDEYTKLLHDGQPVAADIIDSNFASPTYTPRSLPEDDTSMAILSMQDMNFNNYK	613		
DB	575	HMKVSDDEYTKLLHDGQPVAADIIDSNFASPTYTPRSLPEDDTSMAILSMQDMNFNNYK	634		
QY	614	IDCPTLARFLCMVKCKGYRDPYPYNMHAFSVSHFCYLLYKNLELTNYLEDMEIFALPFI SC	673		
DB	635	IDCPTLARFLCMVKCKGYRDPYPYNMHAFSVSHFCYLLYKNLELTNYLEDMEIFALPFI SC	694		
QY	674	MCCHLDHRGTNNSPQVASKSVLAALYSSEGVSVMERHHIPAQAIALINTHGNCNIPDHFRSKD	733		
DB	695	MCCHLDHRGTNNSPQVASKSVLAALYSSEGVSVMERHHIPAQAIALINTHGNCNIPDHFRSKD	754		
QY	734	YQRMLDLMWRDI ILATDLAHLRI PKDJQKMAEVGYDRTNKHHSLLLCLLMTSCDLSDOT	793		
DB	755	YQRMLDLMWRDI ILATDLAHLRI PKDJQKMAEVGYDRTNKHHSLLLCLLMTSCDLSDOT	814		
QY	794	KGWKTRTKIAELIYKEPFSCODLEKANGNRPMENMDREKAYIPBLOJFSFMHEHTAMPTYIKL	853		

Db 95 EEPHELPEQEGKVRNAVSRKRLGCGNGLPGSDLPGLARLVAPLAPDTQVLIPLVDKE 154  
Qy 134 AGAVAAVILVHCGQLSDNEEWSLQAVEKHITLVALKRVQALQORRESSVAPEATONPPBEAA 193  
Db 155 AGAVAAVILVHCGQLSDNEEWSLQAVEKHITLVALKRVQALQORRESSVAPEATONPPBEAA 214  
Qy 194 GDQGGVAYTQDDRKILOLCCBELYDLDASSLQLKVLQYLQOSTQASRCCLLLVSEDNLQL 253  
Db 215 GDQGGVAYTQDDRKILOLCCBELYDLDASSLQLKVLQYLQOSTQASRCCLLLVSEDNLQL 274  
Qy 254 SKCVIGDKVLEEEISFPITTRGLQGVVEDKKSIIQLKDLTSDMQOQLQSMLGCEVQAMLCV 313  
Db 275 SKCVIGDKVLEEEISFPITTRGLQGVVEDKKSIIQLKDLTSDMQOQLQSMLGCEVQAMLCV 334  
Qy 314 PVISRATQVVALACAFNKLGGDLFTDQDEHVIQHCFFHYTSTVLTSTLAFQKOKLKCEC 373  
Db 335 PVISRATQVVALACAFNKLGGDLFTDQDEHVIQHCFFHYTSTVLTSTLAFQKOKLKCEC 394  
Qy 374 QALLQVAKNLFTHLDDVSVLQEIITEARNLSNAEICSVFLLDONELVAKVFDGCVVEDE 433  
Db 395 QALLQVAKNLFTHLDDVSVLQEIITEARNLSNAEICSVFLLDONELVAKVFDGCVVEDE 454  
Qy 434 SYEIRIPADQGIAGHVATTGQILNIPDAYAHPLFYRGVDDSTGFRTRNLCFPIKNENQE 493  
Db 455 SYEIRIPADQGIAGHVATTGQILNIPDAYAHPLFYRGVDDSTGFRTRNLCFPIKNENQE 514  
Qy 494 VIGVAELVNKINGPWFSDDELATAFSIYCGISIAHSLLYKKVNEAQYRSHLANEMMY 553  
Db 515 VIGVAELVNKINGPWFSDDELATAFSIYCGISIAHSLLYKKVNEAQYRSHLANEMMY 574  
Qy 554 HMKVSDDEYTKLLHDGIQPVAAIDSNFASFTYTPRSLPEDDTSMALLSMLQDMNFINNYK 613  
Db 575 HMKVSDDEYTKLLHDGIQPVAAIDSNFASFTYTPRSLPEDDTSMALLSMLQDMNFINNYK 634  
Qy 614 IDCPTLARFCLMVKKGYRDPYPHNWMAFSVSHFCYLLYKNLELTNYLEDMEIFALFISC 673  
Db 635 IDCPTLARFCLMVKKGYRDPYPHNWMAFSVSHFCYLLYKNLELTNYLEDMEIFALFISC 694  
Qy 674 MCHDLDRHGTNNSFQVASKSVLAALYSSEGVSMEHHPAQAIAILNTHGCMIFDHFSRKD 733  
Db 695 MCHDLDRHGTNNSFQVASKSVLAALYSSEGVSMEHHPAQAIAILNTHGCMIFDHFSRKD 754  
Qy 734 YQRMDLMDRIILATDLAHLRIIPKLOKMAEVGYDRTNKOHHSILLCCLMTSCDLSQDT 793  
Db 755 YQRMDLMDRIILATDLAHLRIIPKLOKMAEVGYDRTNKOHHSILLCCLMTSCDLSQDT 814  
Qy 794 KGWKTTRKIAELIYKEFFSQGDLEKAMGNRPMEMMDREKAYIPELQISFMEHIAMPIYKL 853  
Db 815 KGWKTTRKIAELIYKEFFSQGDLEKAMGNRPMEMMDREKAYIPELQISFMEHIAMPIYKL 874  
Qy 854 LQDLFPKAAELYERVASNREHWTKVSHKFTIRGLPSNNSLDFLDBEYVDPDLGARAPIN 913  
Db 875 LQDLFPKAAELYERVASNREHWTKVSHKFTIRGLPSNNSLDFLDBEYVDPDLGARAPIN 934  
Qy 914 GCCSLDAE 921  
Db 935 GCCSLDAE 942

GenCore version 5.1.6  
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OM protein - protein search, using sw model

Run on: June 26, 2005, 12:06:56 ; Search time 128.535 Seconds  
(without alignments)  
3669.244 Million cell updates/sec

Title: US-10-697-894-39  
Perfect score: 4781  
Sequence: 1 MRQPAASRDLPAGEPVPPG.....VPDLGARAPINGCCSLDAE 921

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 1612378 seqs, 512079187 residues

Total number of hits satisfying chosen parameters: 1612378

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database : UniProt\_03.\*

1: uniprot\_eprot.\*

2: uniprot\_trembl.\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

# SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	4781	100.0	921	1	161099 bos taurus
2	4474.5	93.6	941	1	000408 homo sapien
3	4466.5	93.4	941	2	081w54 homo sapien
4	4426	92.6	916	1	Q922s4 mus musculus
5	4324.5	90.5	928	1	Q01062 rattus norv
6	3229	67.5	685	2	Q62mr1 homo sapien
7	1661	34.7	819	2	Q96076 ephydratia f
8	1236	25.9	491	2	Q7q4a0 anopheles g
9	992	20.7	1544	2	Q8mgw0 drosophila
10	991	20.7	934	2	Q9hcr9 homo sapien
11	991	20.7	988	2	Q96s76 homo sapien
12	991	20.7	1018	2	Q95tw8 drosophila
13	991	20.7	1131	2	Q9vfi9 drosophila
14	983	20.6	1365	2	Q9vj79 drosophila
15	979	20.5	935	2	Q8vid6 rattus norv
16	945	19.8	1088	2	Q7qb99 anopheles g
17	938	19.6	856	2	Q65zc7 caenorhabdi
18	938	19.6	859	1	P30645 caenorhabdi
19	924	19.3	883	2	Q6s9e8 rattus norv
20	920.5	19.3	684	2	Q9gzy7 homo sapien
21	917.5	19.2	852	2	Q6s9e9 rattus norv
22	916.5	19.2	779	2	Q6fxx1 homo sapien
23	916	19.2	789	2	Q9ulw9 homo sapien
24	915	19.1	794	2	Q9gyj6 rattus norv
25	914.5	19.1	779	1	Q9v233 homo sapien
26	913.5	19.1	788	2	Q9gyj5 rattus norv
27	909	19.0	796	2	Q6sc21 mus musculus
28	908	19.0	843	2	Q7zw87 brachydantio
29	907.5	19.0	773	2	Q7tpg1 mus musculus
30	907.5	19.0	779	2	Q9wv11 mus musculus
31	907.5	19.0	790	2	Q8ca95 mus musculus

32	907.5	19.0	797	2	Q7TPG2	Q7tpg2 mus musculus
33	906.5	19.0	685	2	Q8VID7	Q8vid7 rattus norv
34	902	18.9	714	2	Q6S9E7	Q6s9e7 rattus norv
35	901	18.8	653	2	Q6S9E6	Q6s9e6 rattus norv
36	900	18.8	714	2	Q9HCP9	Q9hcp9 homo sapien
37	897	18.8	657	2	Q9NTV4	Q9ntv4 homo sapien
38	845.5	17.7	576	2	Q9HB46	Q9hb46 homo sapien
39	841.5	17.6	581	2	Q8VID8	Q8vid8 rattus norv
40	819.5	17.1	854	1	CNRB_HUMAN	P35913 homo sapien
41	803.5	16.8	865	1	CNSA_CANFA	O77746 canis famil
42	801	16.8	875	1	CNSA_HUMAN	O76074 bos taurus
43	799.5	16.7	853	1	CNRB_BOVIN	P23439 bos taurus
44	799.5	16.7	862	1	CNRC_CHICK	P52731 gallus gall
45	797	16.7	856	1	CNRB_CANFA	P33726 canis famil

## ALIGNMENTS

RESULT 1  
ID CN2A\_BOVIN STANDARD; PRT; 921 AA.  
AC P14059; Q28064;  
DT 01-JAN-1990 (Rel. 13, Created)  
DT 01-DEC-1992 (Rel. 24, Last sequence update)  
DE CGMP-dependent 3',5'-cyclic phosphodiesterase (EC 3.1.4.17) (Cyclic  
DE GMP stimulated phosphodiesterase) (CGS-PDE) (CGSPDE).  
GN Name=PDE2A;  
OS Bos taurus (Bovine).  
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
OC Mammalia; Eutheria; Cetartiodactyla; Ruminantia; Pecora; Bovidae;  
OC Bovinae; Bos.  
OX NCBI\_TaxID=9913;  
RN [1]  
RP SEQUENCE FROM N.A. (ISOFORM PDE2A1).  
RX MEDLINE=91373395; PubMed=1654333;  
RA Sonnenburg W.K., Mullaney P.J., Beavo J.A.;  
RT "Molecular cloning of a cyclic GMP-stimulated cyclic nucleotide  
RT phosphodiesterase cDNA. Identification and distribution of isozyme  
RT variants".  
RL J. Biol. Chem. 266:17655-17661 (1991).  
RN [2]  
RP SEQUENCE FROM N.A. (ISOFORM PDE2A3).  
RX TISSUE=Brain;  
RA Juilfs D.M., Sonnenburg W.K., Seraji S., Beavo J.A.;  
RL Submitted (FEB-1996) to the EMBL/GenBank/DBJ databases.  
RN [3]  
RP SEQUENCE OF 592-921 FROM N.A.  
RX TISSUE=Heart;  
RA le Trong H., Beier N., Sonnenburg W.K., Stroop S.D., Walsh K.A.,  
RA Beavo J.A., Charbonneau H.;  
RT "Amino acid sequence of the cyclic GMP stimulated cyclic nucleotide  
RT phosphodiesterase from bovine heart."  
RL Biochemistry 29:10280-10288 (1990).  
RN [4]  
RP SEQUENCE OF 613-694 AND 808-868.  
RX TISSUE=Heart;  
RA Charbonneau H., Beier N., Walsh K.A., Beavo J.A.;  
RT "Identification of a conserved domain among cyclic nucleotide  
RT phosphodiesterases from diverse species".  
RL Proc. Natl. Acad. Sci. U.S.A. 83:9308-9312 (1986).  
CC -!- FUNCTION: Hydrolyzes both cyclic AMP (cAMP) and cyclic GMP (cGMP).  
CC -!- CATALYTIC ACTIVITY: Nucleoside 3',5'-cyclic phosphate + H(2)O =  
CC nucleoside 5'-phosphate.  
CC -!- SUBUNIT: Homodimer.  
CC -!- SUBCELLULAR LOCATION: Membrane-bound (Potential).  
CC -!- ALTERNATIVE PRODUCTS:  
CC Event=Alternative splicing; Named isoforms=3;  
CC Comment=Additional isoforms seem to exist;  
CC Name=PDE2A1;



CC IsoId=O00408-2; Sequence=Not described;  
CC Name=PDE2A;  
CC IsoId=O00408-3; Sequence=Not described;  
CC -!- TISSUE SPECIFICITY: Expressed in brain and to a lesser extent in  
CC heart, placenta, lung, skeletal muscle, kidney and pancreas.  
CC -!- SIMILARITY: Belongs to the cyclic nucleotide phosphodiesterase  
CC family.  
CC -!- SIMILARITY: Contains 1 GAF domain.  
CC This SWISS-PROT entry is copyright. It is produced through a collaboration  
CC between the Swiss Institute of Bioinformatics and the EMBL outstation -  
CC the European Bioinformatics Institute. There are no restrictions on its  
CC use by non-profit institutions as long as its content is in no way  
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CC or send an email to [license@isb-sib.ch](mailto:license@isb-sib.ch)).  
CC -----  
CC EMBL; U67733; AAC51320.1; --  
CC Genbank; HGNC:8777; PDE2A.  
CC MIM; 602658; --  
CC GO; GO:0004118; P:cgmp-stimulated cyclic-nucleotide phosphodi. . .; TAS.  
DR InterPro; IPR003018; GAF.  
DR InterPro; IPR003607; Met\_phos\_hydro.  
DR InterPro; IPR002073; PDEase.  
DR Pfam; PF01590; GAF; 2.  
DR Pfam; PF00233; PDEase I; 1.  
DR PRINTS; PR00387; PDIESTRASE1.  
DR SMART; SM00065; GAF; 2.  
DR SMART; SM00471; HDC; 1.  
DR PROSITE; PS00126; PDEASE I; 1.  
KW Alternative splicing; cGMP; Hydrolyase; Membrane.  
FT DOMAIN 372 550  
FT DOMAIN 633 891 Catalytic (By similarity).  
SQ SEQUENCE 941 AA; 105716 MW; 9797609B487FD64E CRC64;  
  
Query Match 93.6%; Score 4474.5; DB 1; Length 941;  
Best Local Similarity 94.7%; Pred. No. 3.5e-260;  
Matches 860; Conservative 21; Mismatches 26; Indels 1; Gaps 1;  
  
QY 14 QBPVPGSGDGLQDALLSLGSDVIDVAGLQQAQKSAVLKPKVETVYTLDDGSRSLVC 73  
DB 35 EPPPPPPQCADSLQDALLSLGSDVIDSLQRAVKSAVLPRVETVYTLDDGSRSLVC 94  
QY 74 EBPPELPEQGVKREAVISRKLGCGNLGSPDLPGKPLARLVAFLAPDTQVLVPLVDKE 133  
DB 95 EBPPELPEQGVKREAVISRKLGCGNLGSPDLPGKPLARLVAFLAPDTQVLVPLVDKE 154  
QY 134 AGAVALVILVHCGQLSDNEENSLQAVEKHTLVALKRQVLAQRESSVAPRATNPPEAA 193  
DB 155 AGAVALVILVHCGQLSDNEENSLQAVEKHTLVALKRQVLAQRESSVAPRATNPPEGA 214  
QY 194 GQKGGVAVTNDKTLQCGELXDLDASSLQQLKVLQYLQQTQASRCCLLVSDNLQL 253  
DB 215 EQKGGAAVTDKTLQCGELXDLDASSLQQLKVLQYLQQTQASRCCLLVSDNLQL 274  
QY 254 SKCVIGDKVLEBEISFPPTTGRGQVVEDKSIQLKDLTSDMQQLQSMGLGCEVQAMLCV 313  
DB 275 SKCVIGDKVLEBEISFPPTTGRGQVVEDKSIQLKDLTSDMQQLQSMGLGCEVQAMLCV 333  
QY 314 PVISRATQVVALACAFNKLGGDLFTDQDEHVIQHCFTHTVSTLSTAFQEKQKKEC 373  
DB 334 PVISRATQVVALACAFNKLGGDLFTDQDEHVIQHCFTHTVSTLSTAFQEKQKKEC 393  
QY 374 QALLQVAKNLFTHLDDVSVLLQEIITEARNLSNAETCSVFLDDQNELVAKVDPGGVDE 433  
DB 394 QALLQVAKNLFTHLDDVSVLLQEIITEARNLSNAETCSVFLDDQNELVAKVDPGGVDE 453  
QY 434 SYEIRIPADQGIAGHVAATGQILNIPDAYAHPFLYRGVDDSTGFTRNILCFPIKNEQ 493  
DB 454 SYEIRIPADQGIAGHVAATGQILNIPDAYAHPFLYRGVDDSTGFTRNILCFPIKNEQ 513  
QY 494 VTGVAELVNVKINGPWFSPDEDLATAFSIYCGISIAHSLLYKKVNEAQYRSHLANEMMY 553

DB 514 VTGVAELVNVKINGPWFSPDEDLATAFSIYCGISIAHSLLYKKVNEAQYRSHLANEMMY 573  
QY 554 HMKVSDDEYTKLLHDGIQVAAIDSNFASFTYTPRSLPEDDTSMALSLQDMNFNNYK 613  
DB 574 HMKVSDDEYTKLLHDGIQVAAIDSNFASFTYTPRSLPEDDTSMALSLQDMNFNNYK 633  
QY 614 IDCPILARFCLMVKGGYRDPYHNMWHAFSVSHFCVLLYKNLELTNYLEDMEIFALFISC 673  
DB 634 IDCPILARFCLMVKGGYRDPYHNMWHAFSVSHFCVLLYKNLELTNYLEDMEIFALFISC 693  
QY 674 MCHDLDRGTNNNSFVASKSVLAALYSRSGSVWERHHPAQAIATLNTGHCNIFDHF SRKD 733  
DB 694 MCHDLDRGTNNNSFVASKSVLAALYSRSGSVWERHHPAQAIATLNTGHCNIFDHF SRKD 753  
QY 734 YQRMDLMDRIILATDLAHLRFKDLQKMAEYGVYDRTNKQHSLLLCLLMTSCDLSQDT 793  
DB 754 YQRMDLMDRIILATDLAHLRFKDLQKMAEYGVYDRTNKQHSLLLCLLMTSCDLSQDT 813  
QY 794 KGWKTRKIAELIYKEFFSQGLKAMGNRPNEMDMREKAYIPELOISPMHIAMPIYKL 853  
DB 814 KGWKTRKIAELIYKEFFSQGLKAMGNRPNEMDMREKAYIPELOISPMHIAMPIYKL 873  
QY 854 LODLPKAAELYERVASNRHWTYKSHKFTIRGLPSNNSLDFLDREYVDPDLDGARAPIN 913  
DB 874 LODLPKAAELYERVASNRHWTYKSHKFTIRGLPSNNSLDFLDREYVDPDLDGARAPIN 933  
QY 914 GCCSLDAE 921  
DB 934 GCCSLDAE 941  
  
RESULT 3  
Q8IW54  
ID Q8IW54 PRELIMINARY; PRT; 941 AA.  
AC Q8IW54;  
DT 01-MAR-2003 (TrEMBLrel. 23, Created)  
DT 01-MAR-2003 (TrEMBLrel. 23, Last sequence update)  
DT 01-MAR-2004 (TrEMBLrel. 26, Last annotation update)  
DE Phosphodiesterase 2A, cGMP-stimulated.  
GN Name=PDE2A;  
OS Homo sapiens (Human)  
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.  
OX NCBI\_TaxID=9606;  
RN [1]  
RP SEQUENCE FROM N.A.  
RC TISSUE=Brain;  
RX MEDLINE=23388257; PubMed=12477932; DOI=10.1073/pnas.242603899;  
RA Strausberg R.D., Feingold E.A., Grouse L.H., Derge J.G.,  
RA Klausner R.D., Collins F.S., Wagner L., Shenmen C.M., Schuler G.D.,  
RA Altschul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,  
RA Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J., Haieh F.,  
RA Diatchenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L.,  
RA Stapleton M., Soares M.B., Bonaldo M.P., Casavant T.L., Scheetz T.E.,  
RA Brownstein M.J., Udwin T.B., Toshiyuki S., Carninci P., Prange C.,  
RA Raha S.S., Loquellano N.A., Peters G.J., Abramson R.D., Mulláhy S.J.,  
RA Bosak S.A., McEwan P.J., McKernan K.J., Malek J.A., Gunaratne P.H.,  
RA Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,  
RA Villalon D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A.,  
RA Fahey J., Helton E., Kettman M., Shevchenko Y., Bouffard G.G.,  
RA Whiting M., Madan A., Young A.C., Shavchenko Y., Bouffard G.G.,  
RA Blakesley R.W., Touchman J.W., Green E.D., Dickson M.C.,  
RA Rodriguez A.C., Grinchwood J., Schmitz J., Myers R.M., Butterfield Y.S.,  
RA Krzywinski M.I., Skalska U., Smallos D.E., Schnerch A., Schein J.E.,  
RA Jones S.J., Marra M.A.;  
RT "Generation and initial analysis of more than 15,000 full-length human  
RT and mouse cDNA sequences."  
RL Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903 (2002).  
[2]  
RP SEQUENCE FROM N.A.  
RC TISSUE=Brain;  
RA Strausberg R.;  
RL Submitted (DEC-2002) to the EMBL/GenBank/DBSJ databases.





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CC -----  
CC EMBL; BC006845; AAH06845.1; -;  
CC DR EMBL; BC029810; AAH29810.1; -;  
CC DR EMBL; BC057029; -; NOT\_ANNOTATED\_CDS.  
CC DR PDB; 1MCO; X-ray; -;  
CC DR MGD; MGI:2446107; Pde2a.  
CC DR InterPro; IPR002073; PDease.  
CC DR Pfam; PF00233; PDease\_1; 1.  
CC DR PRINTS; PR00387; PDIERSTERASE1.  
CC DR PROSITE; PS00126; PDEASE\_1; 1.  
CC KW 3D-structure; cGMP, Hydrolase; Membrane.  
CC FT DOMAIN 348 526 GAP.  
CC FT DOMAIN 609 867 Catalytic (By similarity).  
CC FT SITE 421 422 GMP binding.  
CC FT BINDING 407 407 GMP.  
CC SQ SEQUENCE 916 AA; 103287 MW; 51C03B08663BF20 CRC64;  
  
Query Match 92.6%; Score 4426; DB 1; Length 916;  
Best Local Similarity 92.1%; Pred. No. 2.7e-257;  
Matches 846; Conservative 35; Mismatches 34; Indels 4; Gaps 1;  
  
QY 1 MRRQPAASRDLPFAQEPVPPGSGDGLQDALLSGVSDVAGLQQAQVKEALSAVLPKVTY 60  
DB 1 MRRQPAASQDPLAQKPEPPGSRDRLLEDALLSGAVIDVAGLQQAQVKEALSAVLPKVTY 60  
  
QY 61 YTYLLDGSRLVCEPPELPOGKREAVISGRKLCNGLGSPDLPGKPLARLVAPLAP 120  
DB 61 YTYLLDGSRLVCEPPELPOGKREAVISGRKLCNGLGSPDLPGKPLARLVAPLAP 120  
  
QY 121 DTQVLVPLVDKAGAAVAVILVHCQSLDNEWSLQAVEKHTLVALKRVQALQRESSV 180  
DB 121 DMQVLVPLVDKAGAAVAVILVHCQSLDNEWSLQAVEKHTLVALKRVQALQRESSV 180  
  
QY 181 APEATONPPEBAAGOKGVAVTNQDRKILQCGELYDLDASSLQKVLQYLOQETQASR 240  
DB 178 -PEAVQNTSVDAESQDKSGYTDHDKILQCGELFDLDATSLQKVLQYLOQETQATH 236  
  
QY 241 CCLLVSEDNQLQCKVIGDKVLEERISPLTTGRLGVQVDEKKSITQLKDLNSEDMLQQL 300  
DB 237 CCLLVSEDNQLQCKVIGDKVLEERISPLTTGRLGVQVDEKKSITQLKDLNSEDMLQQL 296  
  
QY 301 SMLGCEVQAMLCVPVISRATDQVALACAFNKLGGDLFTDQDEHVIQCHFYHTSTVLST 360  
DB 297 NMLGCEVQAMLCVPVISRATDQVALACAFNKLGGDLFTDQDEHVIQCHFYHTSTVLST 356  
  
QY 361 LAFQKEQKLCBCQALLQVAKNLFTHLDDVSVLLQEIITEARNLSNAEICSVFLLDQNEL 420  
DB 357 LAFQKEQKLCBCQALLQVAKNLFTHLDDVSVLLQEIITEARNLSNAEICSVFLLDQNEL 416  
  
QY 421 VAKVFDGGVDESEVIRIPADQAGHATGQILNTPDAYAHPLFVRGVDDSTGFRTR 480  
DB 417 VAKVFDGGVDESEVIRIPADQAGHATGQILNTPDAYAHPLFVRGVDDSTGFRTR 476  
  
QY 481 NILCPFIKNENQEVIGVAVLNKINGPWSKEDDLATAFYSYIGISIAHSLLYKKVNEA 540  
DB 477 NILCPFIKNENQEVIGVAVLNKINGPWSKEDDLATAFYSYIGISIAHSLLYKKVNEA 536  
  
QY 541 QYRSHLANEMMYHMKVSDEYTKLLHDGIQPVAIDSNFASFTYTPRSLPDDTSMAIL 600  
DB 537 QYRSHLANEMMYHMKVSDEYTKLLHDGIQPVAIDSNFANFTYTPRSLPDDTSMAIL 596  
  
QY 601 SMLQDMFNINNYKIDCPTLARCLMVKGYRDPYPHNWHAFFSVSHFCVLLYKNELENY 660  
DB 597 SMLQDMFNINNYKIDCPTLARCLMVKGYRDPYPHNWHAFFSVSHFCVLLYKNELENY 656  
  
QY 661 LEDMEIFALFISCMCHDLDRGTNNNSFQVASKSVLAALYSFGSVYMERHHPAQATAILNT 720  
DB 657 LEDMEIFALFISCMCHDLDRGTNNNSFQVASKSVLAALYSFGSVYMERHHPAQATAILNT 716  
  
QY 721 HGCNIFDHFPSRKDYQRMMLDMRDIILATDLAHLIRIFKDLQKMAEYGVYDNRNQHRLLL 780

DB 717 HGCNIFDHFPSRKDYQRMMLDMRDIILATDLAHLIRIFKDLQKMAEYGVYDNRNQHRLLL 776  
QY 781 CLLMTSCDLSQDTKGWTKTRKIAELIYKEFFSQGDLKAMGNRPMEMMDREKAYIPELQI 840  
DB 777 CLLMTSCDLSQDTKGWTKTRKIAELIYKEFFSQGDLKAMGNRPMEMMDREKAYIPELQI 836  
QY 841 SFEHIAMPIYKLLQDLPPKAAELVYASNEHHTKUSHKFTIRGLPSNNSLDPLDEEY 900  
DB 837 SFEHIAMPIYKLLQDLPPKAAELVYASNEHHTKUSHKFTIRGLPSNNSLDPLDEEY 896  
QY 901 EYVDDLGGARAPINGCCSLD 919  
DB 897 EYVDDLGGARAPINGCCSLD 915  
  
RESULT 5  
CN2A RAT STANDARD; PRT; 928 AA.  
ID CN2A RAT Q01062;  
AC Q01062;  
DT 01-APR-1993 (Rel. 25, Created)  
DT 01-OCT-1996 (Rel. 34, Last sequence update)  
DT 05-JUL-2004 (Rel. 44, Last annotation update)  
DE cGMP-dependent 3',5'-cyclic phosphodiesterase (EC 3.1.4.17) (Cyclic  
GMP stimulated phosphodiesterase) (CGS-PDE) (CGSPDE).  
DE Name=Pde2a;  
GN Rattus norvegicus (Rat).  
OS Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Rattus.  
OX NCBI\_TaxID=10116;  
RN [1]  
RP SEQUENCE FROM N.A.  
RC STRAIN=Sprague-Dawley; TISSUE=Brain;  
RX MEDLINE=95110334; PubMed=7811274;  
RA Yang Q., Paskind M., Bolger G., Thompson W.J., Repaske D.R.,  
RA Cutler L.S., Epstein P.M.;  
RT "A novel cyclic GMP stimulated phosphodiesterase from rat brain.";  
RL Biochem. Biophys. Res. Commun. 205:1850-1858(1994).  
RN [2]  
RP SEQUENCE OF 643-759 FROM N.A.  
RX MEDLINE=92406782; PubMed=1326532;  
RA Repaske D.R., Swinnen J.V., Jin S.L.C., van Wyk J.J., Conti M.;  
RT "A polymerase chain reaction strategy to identify and clone cyclic  
nucleotide phosphodiesterase cDNAs. Molecular cloning of the cDNA  
encoding the 63-kDa calmodulin-dependent phosphodiesterase.";  
RL J. Biol. Chem. 267:18683-18688(1992).  
CC - FUNCTION: Hydrolyzes both cyclic AMP (cAMP) and cyclic GMP (cGMP).  
CC - CATALYTIC ACTIVITY: Nucleoside 3',5'-cyclic phosphate + H(2)O =  
nucleoside 5'-phosphate.  
CC - SUBUNIT: Homodimer (By similarity).  
CC - SUBCELLULAR LOCATION: Membrane-bound (Potential).  
CC - ALTERNATIVE PRODUCTS:  
CC Event-Alternative splicing; Named isoforms=3;  
CC Comment=Additional isoforms seem to exist. Experimental  
confirmation may be lacking for some isoforms;  
CC Name=PDE2A3;  
CC IsoId=Q01062-1; Sequence=Displayed;  
CC Name=PDE2A1;  
CC IsoId=Q01062-2; Sequence=Not described;  
CC Name=PDE2A2;  
CC IsoId=Q01062-3; Sequence=Not described;  
CC - TISSUE SPECIFICITY: Brain.  
CC - SIMILARITY: Belongs to the cyclic nucleotide phosphodiesterase  
family.  
CC - SIMILARITY: Contains 1 GAP domain.  
CC -----  
CC This SWISS-PROT entry is copyright. It is produced through a collaboration  
between the Swiss Institute of Bioinformatics and the EMBL outstation -  
the European Bioinformatics Institute. There are no restrictions on its  
use by non-profit institutions as long as its content is in no way  
modified and this statement is not removed. Usage by and for commercial  
entities requires a license agreement (See <http://www.isb-sib.ch/announce/>  
or send an email to [license@isb-sib.ch](mailto:license@isb-sib.ch)).

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DR EMBL; U211101; AAA63683.1; -.
DR EMBL; M94540; AAA40922.1; -.
DR PIR; JC2486; JC2486.
DR RGD; 620965; Pde2a.
DR InterPro; IPR003018; GAF.
DR InterPro; IPR003607; Met_phos_hydro.
DR InterPro; IPR002073; PDEase.
DR Pfam; PF01590; GAF; 2.
DR Pfam; PF00233; PDEase_I; 1.
DR PRINTS; PR00387; PD1ESTERASE1.
DR SMART; SM00065; GAF; 3.
DR SMART; SM00471; HDC; 1.
DR PROSITE; PS00126; PDEASE_I; 1.
KW Alternative splicing; cGMP; Hydrolase; Membrane.
FT DOMAIN 360 538
FT DOMAIN 621 879
FT CONFLICT 646 646 W -> R (in Ref. 2).
FT CONFLICT 758 758 L -> M (in Ref. 2).
SQ SEQUENCE 928 AA; 104663 MW; EF0B8C1E266EAB18 CRC64;

Query Match 90.5%; Score 4324.5; DB 1; Length 928;
Best Local Similarity 91.7%; Pred. No. 3.5e-251;
Matches 830; Conservative 32; Mismatches 38; Indels 5; Gaps 2;

Qy 15 BPVPPGSGDQALQDALLSLGSLVDVAGLQQAQKAEALSAVLPKVTYVTVYLLDGSRLVCE 74
Db 28 EPPQPACADSLQDALLSLGSLVDVAGLQQAQKAEALSAVLPKVTYVTVYLLDGSRLVCE 86
Qy 75 EPPHELPOEGKVREAVISRKLGCNGLGSPDLPGKPLARLVLAPDPTQVLVPLVDKEA 134
Db 87 DPPHELPOEGKIREAVISRKLSCDGLGSPDLLGKPLARLVLAPDPTQVLVPLVDKET 146
Qy 135 GAVAAVLVHCGQLSDNEEWSLQAVEKTVLALVKRQALQRESVAPETQNPPEAAG 194
Db 147 GTVAARVLVHCGQLSDSEQLQVVEKHALVALQVQALQRR----PEAVQNTSADPSE 202
Qy 195 DQKGVATYNDRKTLQLCGLYDLDASSLQQLKVLYQQEQTQASRCCLLLVSDNQLS 254
Db 203 DQKEGYTADRKLQLCGLYDLDASSLQQLKVLYQQEQTQATHCCLLLVSDNQLS 262
Qy 255 CKVIGDKYLEBEISPLTTLGQVVEDKSIQLKDLTSDMQQLQSMGLGEVQAMLCVP 314
Db 263 CKVIGEKVLGEVSFPLTMGRLGQVVEDKQCIQLKDLTSDVQQLQNMGLGELRAMLCVP 322
Qy 315 VISRATDQVALACAFNKLGDGLFTDQDEHVIQCFHYTSTVLTSLAFQEKQLKCECQ 374
Db 323 VISRATDQVALACAFNKLGDGLFTDQDERAIOHCFHYTGTVLTSLAFQEKQLKCECQ 382
Qy 375 ALLQVAKNLFTHLDDVSLVLLQEIITEARNLSNAEICSVFLLDQNELVAKVFDGGVDEES 434
Db 383 ALLQVAKNLFTHLDDVSLVLLQEIITEARNLSNAEICSVFLLDQNELVAKVFDGGVDDDES 442
Qy 435 YEIRIPADQGIAGHVATTGQILNPIDAYAHPLFYRGVDDSTGFRTRNLICFPPIKNQEV 494
Db 443 YEIRIPADQGIAGHVATTGQILNPIDAYAHPLFYRGVDDSTGFRTRNLICFPPIKNQEV 502
Qy 495 IGVAELVNKINGPWFSEKDEDLATAFSYCGISIAHSLLYKKVNEAQYRSHLANEMMYH 554
Db 503 IGVAELVNKINGPWFSEKDEDLATAFSYCGISIAHSLLYKKVNEAQYRSHLANEMMYH 562
Qy 555 MKVSDDEVTKLLHGGIQPVAIDSNFASFTYTPRSLPEDDTSMALLSMLQDMNFINNYKI 614
Db 563 MKVSDDEVTKLLHGGIQPVAIDSNFANFTYTPRSLPEDDTSMALLSMLQDMNFINNYKI 622
Qy 615 DCPTLARFCLMVKGYRDPYPYHNMHAFSVSHFCYLLKNTLYLEDMEIFALFISCM 674
Db 623 DCPTLARFCLMVKGYRDPYPYHNMHAFSVSHFCYLLKNTLYLEDMEIFALFISCM 682
Qy 675 CHDLDRGTNNSFQVASKSVLAALYSSEGSVWERHHPAQAIALLNTHGCNIFDHFSCRDY 734
Db 683 CHDLDRGTNNSFQVASKSVLAALYSSEGSVWERHHPAQAIALLNTHGCNIFDHFSCRDY 742
Qy 735 QRMLDLMRDIIATDLAHLRI FKDLQKQAEVGYDRNNKQHRLLLCLLMTSCDLSQDTK 794
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Db 743 QRMLDLMRDIIATDLAHLRI FKDLQKQAEVGYDRNNKQHRLLLCLLMTSCDLSQDTK 802
Qy 795 GWKTRKIAELIYKEPFSQGDLEKAMGNRPENMDREKAYIPELQISPMEHAMPIYKLL 854
Db 803 GWKTRKIAELIYKEPFSQGDLEKAMGNRPENMDREKAYIPELQISPMEHAMPIYKLL 862
Qy 855 QDLFPKAAELYERVASNREHWTKVSHKFTIRGLPSNNSLDFLDEEYEVDPDLDGARAPNG 914
Db 863 QDLFPKAAELYERVASNREHWTKVSHKFTIRGLPSNNSLDFLDEEYEVDPDLDTVRAPNG 922
Qy 915 CCSLD 919
Db 923 CCSLE 927

RESULT 6
Q6ZMR1
ID Q6ZMR1 PRELIMINARY; PRT; 685 AA.
AC Q6ZMR1;
DT 05-JUL-2004 (TrEMBLrel. 27, Created)
DT 05-JUL-2004 (TrEMBLrel. 27, Last sequence update)
DT 05-JUL-2004 (TrEMBLrel. 27, Last annotation update)
DE Hypothetical protein FLJ16750.
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX NCBI_TaxID=9606;
RN [1]
SEQUENCE FROM N.A.
RC TISSU=Adrenal gland;
RA Tanigami A., Fujiwara T., Shibahara T., Goto Y., Hirao M., Shimizu F.,
RA Wakebe H., Ono T., Hishigaki H., Watanabe T., Ozaki K., Sugiyama T.,
RA Irie R., Otsuki T., Sato H., Ota T., Wakamatsu A., Ishii S.,
RA Yamamoto J., Isono Y., Kawai-Hio Y., Saito K., Nishikawa T.,
RA Kimura K., Yamashita H., Matsuo K., Nakamura Y., Sekine M.,
RA Kikuchi H., Kanda K., Wagatsuma M., Murakawa K., Kanehori K.,
RA Takahashi-Fujii A., Oshima A., Sugiyama A., Kawakami B., Suzuki Y.,
RA Sugano S., Nagahara K., Masuho Y., Nagai K., Isogai T.;
RL Submitted (MAR-2004) to the EMBL/GenBank/DBJ databases.
DR EMBL; AK131525; BADI8664.1; -.
DR GO; GO:0004114; F:3';5'-cyclic-nucleotide phosphodiesterase a. . .; IEA.
DR GO; GO:0003824; F:catalytic activity; IEA.
DR GO; GO:0007165; P:signal transduction; IEA.
DR InterPro; IPR003018; GAF.
DR InterPro; IPR003607; Met_phos_hydro.
DR InterPro; IPR002073; PDEase.
DR Pfam; PF01590; GAF; 1.
DR PRINTS; PR00387; PD1ESTERASE1.
DR SMART; SM00065; GAF; 1.
DR SMART; SM00471; HDC; 1.
DR PROSITE; PS00126; PDEASE_I; 1.
SQ SEQUENCE 685 AA; 78177 MW; A6087394B98221C3 CRC64;

Query Match 67.5%; Score 3229; DB 2; Length 685;
Best Local Similarity 70.2%; Pred. No. 1.6e-185;
Matches 637; Conservative 11; Mismatches 10; Indels 250; Gaps 1;

Qy 14 QEPVPPSGDQALQDALLSLGSLVDVAGLQQAQKAEALSAVLPKVTYVTVYLLDGSRLVCE 73
Db 28 EPPQPACADSLQDALLSLGSLVDVAGLQQAQKAEALSAVLPKVTYVTVYLLDGSRLVCE 87
Qy 74 EPPHELPOEGKVREAVISRKLGCNGLGSPDLPGKPLARLVLAPDPTQVLVPLVDKE 133
Db 88 EDPHELPOEGKVR----- 101
Qy 134 AGAVAAVLVHCGQLSDNEEWSLQAVEKTVLALVKRQALQRESVAPETQNPPEAAG 193
Db 102 ----- 101
Qy 194 GDQKGVATYNDRKTLQLCGLYDLDASSLQQLKVLYQQEQTQASRCCLLLVSDNQL 253
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Db 102 ----- 101  
Qy 254 SKVIGDKVLEEISFPLTTGRLGVVDKKSILQKLTSDMQOOLQSLGCEVQAMLCV 313  
Db 102 ----- 101  
Qy 314 PVISRATQVVALACAFNKLGGDLFTDQDEHVIQHCFTYTTSTLTAFQEKQKKEC 373  
Db 102 ----- 101  
Qy 374 QALLQVAKNLFTHLDDVSVLLQEIITEARNISNAEICSVELLDQNELVAKVDFGCVVDE 433  
Db 138 QALLQVAKNLFTHLDDVSVLLQEIITEARNISNAEICSVELLDQNELVAKVDFGCVVDE 197  
Qy 434 SYEIRIPADQGIAGHVATTGQILNIPDAYHPLFYRGVDDSTGFRTRNLCFFIKENQOE 493  
Db 198 SYEIRIPADQGIAGHVATTGQILNIPDAYHPLFYRGVDDSTGFRTRNLCFFIKENQOE 257  
Qy 494 VIGVAVELVKNKINGPWFSEDEDLATAFSIYCGISIAHSLLYKKVNEAQYRSHLANEMMY 553  
Db 258 VIGVAVELVKNKINGPWFSEDEDLATAFSIYCGISIAHSLLYKKVNEAQYRSHLANEMMY 317  
Qy 554 HMKVSDDDEYTKLLHDGIVPAAIDSNFASFTYTPESLPEDDTSMALLSMLQDMNFINNYK 613  
Db 318 HMKVSDDDEYTKLLHDGIVPAAIDSNFASFTYTPESLPEDDTSMALLSMLQDMNFINNYK 377  
Qy 614 IDCPTLAFCLMVKKGYRDPYPHNMWHAFFSVSHFCYLLYKNELTNYLEDMEIFALFISC 673  
Db 378 IDCPTLAFCLMVKKGYRDPYPHNMWHAFFSVSHFCYLLYKNELTNYLEDMEIFALFISC 437  
Qy 674 MCHDLDRGTNNSSFOVASKSVLAALYSSEGVSWMERHHPAQIAILNTHGNCIFDHFSKRD 733  
Db 438 MCHDLDRGTNNSSFOVASKSVLAALYSSEGVSWMERHHPAQIAILNTHGNCIFDHFSKRD 497  
Qy 734 YORMLDLMDRIILATDLAHLRIKDLQKMAEVGYDRNKKOHHSLLCCLMTSCDLSQDT 793  
Db 498 YORMLDLMDRIILATDLAHLRIKDLQKMAEVGYDRNKKOHHSLLCCLMTSCDLSQDT 557  
Qy 794 KGWTKTRKIAELIYKEFFSQGDEKAMGNRPMEWMDREKAYIPELQISFMEHIAPIYKL 853  
Db 558 KGWTKTRKIAELIYKEFFSQGDEKAMGNRPMEWMDREKAYIPELQISFMEHIAPIYKL 617  
Qy 854 LODLPKAAELYERVASNRHWTKVSHKFTIRGLPNSNSLDFLDEYEVPLDGRAPIN 913  
Db 618 LODLPKAAELYERVASNRHWTKVSHKFTIRGLPNSNSLDFLDEYEVPLDGRAPIN 677  
Qy 914 GCCSLDAE 921  
Db 678 GCCSLDAE 685

RESULT 7  
Qy 096076 PRELIMINARY; PRT; 819 AA.  
AC 096076;  
DT 01-MAY-1999 (Tremblrel. 10, Created)  
DT 01-MAY-1999 (Tremblrel. 10, Last sequence update)  
DT 01-MAR-2004 (Tremblrel. 26, Last annotation update)  
DE EFPDE2.  
OS Ephydatia fluviatilis.  
OC Eukaryota; Metazoa; Porifera; Demospongiae; Ceractinomorpha;  
OX Haploeclerida; Spongillidae; Ephydatia.  
NCBI TaxID=31330;  
RN [1]\_taxid=31330;  
RP SEQUENCE FROM N.A.  
RX MEDLINE=99015760; PubMed=9801141; DOI=10.1016/S0014-5793(98)01150-8;  
RA Koyanagi M., Suga H., Hoshiyama D., Ono K., Iwabe N., Kuma K.,  
RA Miyata T.;  
RT "Ancient gene duplication and domain shuffling in the animal cyclic  
nucleotide phosphodiesterase family";  
RL FEBS Lett. 436:323-328(1998).  
DR EMBL; AB017022; BAA34308.1; -.  
DR GO; GO:0004114; F:3',5'-cyclic-nucleotide phosphodiesterase a. . .; IEA.

DR GO; GO:0003824; F:catalytic activity; IEA.  
DR GO; GO:0007165; P:signal transduction; IEA.  
DR InterPro; IPR003018; GAF.  
DR InterPro; IPR003607; Met\_phos\_hydro.  
DR InterPro; IPR002073; PDEase.  
DR Pfam; PF01590; GAF; 2. 1.  
DR Pfam; PF00233; PDEase\_1; 1.  
DR PRINTS; PR00387; PDIESTERASE1.  
DR SMART; SM0065; GAF; 2.  
DR SMART; SM00471; HDC; 1.  
DR PROSITE; PS00126; PDEASE\_I; 1.  
SQ SEQUENCE 819 AA; 92145 MW; F4CA1EE8B23A9E0E CRC64;  
Query Match 34.7%; Score 1661; DB 2; Length 819;  
Best Local Similarity 39.9%; Pred. No. 3.5e-91;  
Matches 346; Conservative 161; Mismatches 256; Indels 104; Gaps 10;  
Qy 27 QDALLSGSVLDVAGLQOAVKEALSAPLKVETVTVYLLDGESRLVC---EPPHELPQ 82  
Db 23 EDAILGMAANSPTFTAAAGCLRFTFSSAGVALLDTENNELAYFEENDKVTPLPK 82  
Qy 83 EGVREAVISRKRLGCGNGLSPDLPGKPLARLAPLAPDTQVLTPLVDKEGAAVAIL 142  
Db 83 MGVWDVQR----- 93  
Qy 143 VHCQSLDNEEWSLOAVEKHTLVALKRVQALQORESSVAPEATQNPBEAAGDQGGVAY 202  
Db 94 ---TLEENYE-RLRLLETTVAARKV-----LAH 119  
Qy 203 TNQDRK-----ILQCGELYDLDAASSLQKVLQVLOQETOASRCCLLVSEDNQLQSLCK 256  
Db 120 LNSEHEKRIIDNMLRVCGELIDLDVVSLSIKLKHIMEVSNKAKCTLFYEDVTQELVAY 179  
Qy 257 VIGDKVLEEISFPLTTGRLGVVDKKSILQKLTSDMQ---OLQSLGCEVQAMLCV 313  
Db 180 TYNGVPLDKERKPVSSSIYCECTTGELINISV-PQDMRFPNPRIDIKGVEPTHLICI 238  
Qy 314 PVISR---ATQVVALACAFNKLGGDLFTDQDEHVIQHCFTYTTSTLTAFQEKQK 370  
Db 239 PVKDRGAGQSQSVGLVVCNDKNDRPFTKDEEGLYSLHFCSSMLNNTLVYQRELAK 298  
Qy 371 CECQALLQVAKNLFTHLDDVSVLLQEIITEARNISNAEICSVELLD---QNELVAKVDFG 428  
Db 299 KQNEVLLQVAKNLFTHLDDVSVLLQEIITEARNISNAEICSVELLDKGRSLNVAIVFNGD 358  
Qy 429 VVEDESVEIRPADQGIAGHVATTGQILNIPDAYHPLFYRGVDDSTGFRTRNLCFFIK 488  
Db 359 VLKERTLTIV--GGIAGYVAKGTIVNIIVDAQKHPQFAEVDKSTGFTKHLICFFIM 416  
Qy 489 NENQEVIGVAVELVKNKINGPWFSEDEDLATAFSIYCGISIAHSLLYKKVNEAQYRSHLAN 548  
Db 417 DNGGVVGVAVELCNKINGKFTKYDEELARTFSAYCGISIVHSKLYETVMASQGRSSLAT 476  
Qy 549 EMMYHMKVSDDEYTKLLHDGIVPAAIDSNFASFTYTPESLPEDDTSMALLSMLQDMN 608  
Db 477 ELMYHMKIRPDELERATKTPLPVSSPFHEMCKLTFSPDLKNSADEIAVMNMNMDL 536  
Qy 609 INNVKIDCPTLAFCLMVKKGYRDPYPHNMWHAFFSVSHFCYLLYKNELTNYLEDMEIFA 668  
Db 537 INKFQHPDILARFVIMVKGIRDPYPHNMWHAFFSVHFLYALYCCSKLCLDLEVL 596  
Qy 669 LFIICMCHDLDRGTNNSSFOVASKSVLAALYSSEGVSWMERHHPAQIAILNTHGNCIFDH 728  
Db 597 LFSVCLCHDIDHRTGTTNAFQVCSNSTLACYSSSEGVSWMERHHLAQLTCLINSPGCNIFEN 656  
Qy 729 FSRKDYQRMLDMDRIILATDLAHLRIKDLQKMAEVGYDRNKKOHHSLLCCLMTSCD 788  
Db 657 LSDSDYRTTIQLIQDILDTDIASHLKKLKHIKQWANDGYERSNPEHRLMCSLMTSCD 716  
Qy 789 LSDQTKGWTKTRKIAELIYKEFFSQGDEKAMGNRPMEWMDREKAYIPELQISFMEHIA 848  
Db 717 LTASCKTWESNKAISDLIYQEFFSQGDEKALGVTPSEMDORDRAFIPEQQLQFLDNIA 776

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Qy 849 PIVKLODLFPKAAELYERVASNRHH 875
Db 777 FVYQLLSRLPESAAAHVTLIDNRQW 803

RESULT 8
Q7Q4A0 PRELIMINARY; PRT; 491 AA.
AC Q7Q4A0 (TrEMBLrel. 26, Created)
DT 01-MAR-2004 (TrEMBLrel. 26, Last sequence update)
DT 01-MAR-2004 (TrEMBLrel. 26, Last annotation update)
DE EbiP6713 (Fragment)
GN Name=ebiG6713; ORFNames=ENSANG00000005075;
OS Anopheles gambiae str. FEST.
OC Eukaryota; Metazoa; Arthropoda; Hexapoda; Insecta; Pterygota;
OC Neoptera; Endopterygota; Diptera; Nematocera; Culicoides; Anopheles.
OX NCBI_TaxID=180454;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=PEST;
RA Anopheles Genome Sequencing Consortium;
RL Submitted (MAR-2002) to the EMBL/GenBank/DBJ databases.
CC -! CAUTION: The sequence shown here is derived from an
CC EMBL/GenBank/DBJ whole genome shotgun (WGS) entry which is
CC preliminary data.
DR EMBL; AAB01008964; EAA12229.1; -.
DR GO; GO:0004114; F:3, 5'-cyclic-nucleotide phosphodiesterase a. . .; IEA.
DR GO; GO:0007165; P:signal transduction; IEA.
DR InterPro; IPR003018; GAF.
DR InterPro; IPR002073; PDEase.
DR Pfam; PF01590; GAF; 1.
DR Pfam; PF00233; PDEase_I; 1.
DR PRINTS; PR00387; PDIESTERASE1.
DR PROSITE; PS00126; PDEASE_I; 1.
FT NON_TER 1
FT NON_TER 491
SQ SEQUENCE 491 AA; 56349 MW; 5416132CA4E2F3 CRC64;

Query Match 25.9%; Score 1236; DB 2; Length 491;
Best Local Similarity 50.5%; Pred. No. 5.8e-66;
Matches 250; Conservative 91; Mismatches 138; Indels 16; Gaps 8;

Qy 393 LLQBIITARNLSNAETCSVPILLQON--ELVAKVFDGQVVEDESYETRIPADQGIAGHVA 450
Db 4 LLRGVMTAEKELAAAEKCSFLDKHTGELVSKVFDG---NEASKEIRIESGKGAGYVA 60

Qy 451 TTGQILNIPDAYAHPLFVRGVDSTGPRTRNLCPPIKNENQEVIGVAELVNKINGPWFS 510
Db 61 QTGKLLNIRNAYQHPLFYKGVDESTGFKTRNLCPPICDE--EGVIGVAQLCNKUNGPHFD 119

Qy 511 KFDDELATAFYCGISIAHSLLYKYNQAEQYRHLANEMMYHMKVSDDEYTKLLHDGI 570
Db 120 KCDEVATAFSVYCGISIMHALVHKVQKAEARKYLSQELLLYHMKVPDTEVNHAEAVK 179

Qy 571 QPVAADIS--NFASFTYTPRSLPEDDTSMAL--LSMLQDMFNINNYKIDCPTLAPCLMV 626
Db 180 EPDREQDELTYTFRFPFCPRDVKDHALSVQLAMRMFYDLNFVGSFKIHEYKLFARFVLLV 239

Qy 627 KKGVRDPYNNMHAFSVSHFCYLLYKNLEL--TNYLEDMEIFALFSCMCHDLDRGTN 684
Db 240 QKGRDTPYNNWHAFSVAHFAYSLMNNLRILIERGIITKMGGSFLTAAPCHDLDRGIS 299

Qy 685 NSFQVAKSVLAALYSSEGSVMERHFAQAIALTNHGCNIFDHSRKYQORMDLMDRI 744
Db 300 NSYQTSSPLARYSSEGSVMERHLSQAICILNDSSSKLDGLSTFEKEDYLREL 359

Qy 745 ILATDLAHLRI FKDLQKM--AEVGVDRTNKQHSLILCLMTSCDLSQDTGKWTTKIA 803
Db 360 ILATDLANHFRILPRLKKRAEYLTEGSRQ--LLSLMTITCCDLNDQIKSWKTQHVVA 416

Qy 804 ELIYKEFSQDLKAMGNRMWMDREKAVIPELOISFMHEIAMPYIKLQDLFPKAAE 863
Db 804 ELIYKEFSQDLKAMGNRMWMDREKAVIPELOISFMHEIAMPYIKLQDLFPKAAE 863

Db 417 HLVAEFPFAEGDLEKQMLRPNAMDRKKACIPMLQIEFLTTRVIRPTFEILVQIFPETGS 476
Qy 864 LYERVASNRHHWTKV 878
Db 477 FLDTIDSNRQWERV 491

RESULT 9
Q8MQW0 PRELIMINARY; PRT; 1544 AA.
AC Q8MQW0 (TrEMBLrel. 22, Created)
DT 01-OCT-2002 (TrEMBLrel. 22, Last sequence update)
DT 01-OCT-2002 (TrEMBLrel. 22, Last annotation update)
DE SLL3096p.
GN Name=Pdel1; Synonyms=CG10231;
OS Drosophila melanogaster (Fruit fly).
OC Eukaryota; Metazoa; Arthropoda; Hexapoda; Insecta; Pterygota;
OC Neoptera; Endopterygota; Diptera; Brachycera; Muscomorpha;
OC Ephydroidea; Drosophilidae; Drosophila.
OX NCBI_TaxID=7227;
RN [1]
RP SEQUENCE FROM N.A.
RA Stapleton M., Brokstein P., Hong L., Agbavani A., Carlson J.,
RA Champe M., Chavez C., Dorsett V., Dresnek D., Farfan D., Frise E.,
RA George R., Gonzalez M., Guarin H., Krommiller B., Li P., Liao G.,
RA Miranda A., Mungall C.J., Nuncio J., Pacble J., Paragas V., Park S.,
RA Patel S., Phouanavong S., Wan K., Yu C., Lewis S.E., Rubin G.M.,
RA Celniker S.;
RL Submitted (JUN-2002) to the EMBL/GenBank/DBJ databases.
DR EMBL; AY122262; AAM52774.1; -.
DR FlyBase; FBgn0032686; Pdel1.
DR GO; GO:0004114; F:3, 5'-cyclic-nucleotide phosphodiesterase a. . .; IEA.
DR GO; GO:0003824; F:catalytic activity; IEA.
DR GO; GO:0007165; P:signal transduction; IEA.
DR InterPro; IPR003018; GAF.
DR InterPro; IPR003607; Met_phos_hydro.
DR InterPro; IPR002073; PDEase.
DR Pfam; PF01590; GAF; 2.
DR Pfam; PF00233; PDEase_I; 1.
DR PRINTS; PR00387; PDIESTERASE1.
DR SMART; SM00065; GAF; 2.
DR SMART; SM00471; HDC; 1.
DR PROSITE; PS00126; PDEASE_I; 1.
SQ SEQUENCE 1544 AA; 171689 MW; F5254E0CCDB3D065 CRC64;

Query Match 20.7%; Score 992; DB 2; Length 1544;
Best Local Similarity 32.2%; Pred. No. 1.4e-50;
Matches 245; Conservative 147; Mismatches 302; Indels 68; Gaps 19;

Qy 209 ILQCGELYDLDASSLQKLVLYQQETQASRCCLLV-----SEDNLQLSKV----- 257
Db 502 VKDICE--LEVRTLCHKILQNVISILLNADRGSLFLVQGRGCPDGLK-KCLVSKLPDV 557

Qy 258 -----IGDKVLEERI SPLTTGRLGQVVEDKKS1QLKDLTSEDM--QOLQMLGCEVAM 310
Db 558 CPRSTVEEMEQDDSVRVANGTGIAGHVAESGEPNIPDAYODERFNCEDISLTGRTKAL 617

Qy 311 LCVFVISRATDQVVALACAFNKLGGDLFTDQDEHVIQHCFTYTSVLTSTLAFQKEQKLK 370
Db 618 LCPKIDSSGD-VLGVAQVINKNNGECFSEIDEKVFSYLFQFCGILRNAQLYEKSQLLEI 676

Qy 371 CEQALLQVAKNLPHTLDDSVLLQELIITEARNLSNAEICSVFLDDQNE--LVAKVFD-- 426
Db 677 KRNVQLDLARMIPEEQSTIEHVMVFRILTHMQSLIQCRVQVILLVHEADKGSFRVDFPE 736

Qy 427 -GGVVEDS-----YEIRPADOGIAGHVATTCCQILNIPDAYAHPLFYRGVDDSTGPR 479
Db 737 ANDLSEBEARTSPYSRPFNIGITGHVATTGETVNVPNAYEDDRFADSDVENSCEF 796

Qy 480 RNILCFPIKKNENQEVIGVAELVNKINGPWFSKFDDELATAFSIYCGISIAHSLLYKYN 539
Db 797 RSLICMAIKSLGQIIIGVILINKFNELDTFKNDENFVEAFIFCGMGIHNTMYEKAIV 856
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Db 831 AELVTSEFFEQDRERLEKLTPSAIFDRNRKDELPRQLQLEWDSICMPLQALVKVNVK 890
Qy 861 AAEIYERVASNRHWTKVSHKFTIRGLPSNNS 892
Db 891 LKPLMDSVATNRSKWEELHQRLLASTASSSS 922

RESULT 11
Q96S76 PRELIMINARY; PRT; 988 AA.
ID Q96S76;
AC Q96S76;
DT 01-DEC-2001 (TrEMBLrel. 19, Created)
DT 01-DEC-2001 (TrEMBLrel. 19, Last sequence update)
DT 01-MAR-2004 (TrEMBLrel. 26, Last annotation update)
DE Phosphodiesterase 11A3.
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX NCBI_TaxID=9606;
RN [1]
RP SEQUENCE FROM N.A. PubMed=11121118;
RA MEDLINE=20570133; PubMed=11121118;
RX Yusa K., Kanoh Y., Okumura K., Omori K.;
RT "Genomic organization of the human phosphodiesterase PDE11A gene;
RT Evolutionary relatedness with other PDEs containing GAF domains.";
RL Eur. J. Biochem. 268:168-178(2001).
DR EMBL; AB048423; BAB62713.1; JOINED.
DR EMBL; AB048402; BAB62713.1; JOINED.
DR EMBL; AB048403; BAB62713.1; JOINED.
DR EMBL; AB048404; BAB62713.1; JOINED.
DR EMBL; AB048405; BAB62713.1; JOINED.
DR EMBL; AB048406; BAB62713.1; JOINED.
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DR EMBL; AB048419; BAB62713.1; JOINED.
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DR EMBL; AB048422; BAB62713.1; JOINED.
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DR GO; GO:0003824; F:catalytic activity; IEA.
DR GO; GO:0007165; P:signal transduction; IEA.
DR InterPro; IPR003018; GAF.
DR InterPro; IPR003607; Met_phos_hydro.
DR InterPro; IPR002073; PDEase.
DR Pfam; PF01590; GAF; 2.
DR Pfam; PF00233; PDEase I; 1.
DR PRINTS; PR00387; PDESTERASE1.
DR SMART; SM00065; GAF; 2.
DR SMART; SM00471; HDC; 1.
DR PROSITE; PS00126; PDEASE I; 1.
SQ SEQUENCE 988 AA; 111169 MW; 7F678869353DF7BB CRC64;

Query Match 20.7%; Score 991; DB 2; Length 988;
Best Local Similarity 30.8%; Pred. No. 8.4e-51;
Matches 250; Conservative 159; Mismatches 321; Indels 82; Gaps 19;

Qy 143 VHCGLSDNBSWSLQAVSKHTLVALKRVQALQORESSVAP-----EATQNPPE-- 190
Db 185 IHNRTYD-EQVTSRAQEPSSV---RRRLRKASSLPPTAILSLLESRYNLFPQYP 240
Qy 191 EAAGQGGVAYTNQDRKRLQCGEL-YDLDASSLQLKVLQYLOQETOASRCCLLLVSED 249
Db 241 PTADYKCHLKXHNREQFLELVKDISLDLTSLSYKILIFVCLMWADVADRCSLFLV--E 298
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Qy 250 NLQLSCKVIGDKVLE-----EISFPLTTGRLGVVVEDKKSIOIKOLTS 293
Db 299 GAAGKKTIVSKPFDVHAGTPLLPCSSSTENSNEVQVPGKGIIGYVGHGFTVNPDAYQ 358
Qy 294 EDM--QQLQSMGLCEVOAMLCVPVISRATD--QVVALACAFNKL--GGDLFTDDEHVIQHC 349
Db 359 DRRENDEIDKLTGYKTKSLLCMPI--RSSDEIGVQAQAINKIPEGAPFTEDDEKVMQMY 416
Qy 350 PHYTSTVLTSTLAFQKEQKLKCEQALLOVANLFTLDDVSVLLQELIITERNLSNAEI 409
Db 417 LPFCGIAISNAQLFAASKEYERSRALLEVVNDLFBQQTDLKIVKIMHRAQTLLKCR 476
Qy 410 CSVELLDQNELVAKVFGGVVEDSYRIRP-----ADQGIA 446
Db 477 CSVLLLEDIESPVVKF-----TKSFLMSPKCSADAENSFKESMEKSSYSDWLINNSIA 530
Qy 447 GHVATTQOILNPDAYAHPFYRGVDDSTGFRTRNIIICFPKINBNQEVIGVAVELNVKING 506
Db 531 ELVASTGLPVNISDAYQDPRDAEADQISGFHRSVLCVPIWNSNHQIIGVAVLNRLDG 590
Qy 507 PWFSPDEDLATAFSIYCGISIAHSLLYKKVNEAQYRSHLANEMMMHYMKYSDDEYTKLL 566
Db 591 KPFDADQRLFEAFVIFCGLGINNTIMYDQYKSKWAKSQSVALDVLVSHATCSKAEDVKFK 650
Qy 567 HDGIQPVAAI--DSNEASFYTPRSLPEDDTSMAILSMLQDMNFNNYKIDCPTLARFC 623
Db 651 AANIPVSELAIDDIHDDF-----SLDVAWITTAALRMFELGMVQKFKLDYETLCRWL 705
Qy 624 LMVKKGYRDPYPYHNMHAFSVSHFCYLLYKNLENTYLEDMEIFALPFI SCMCHDLDRGT 683
Db 706 LTVKKNYRMVLYHNRHAFNVQCLMPFAMLTAGFDQDILTEVEILAVIVGCLCHDLDRGT 765
Qy 684 NNSFOVASKSVLAALYSSEGSVMRHHFAQAIATLTHGCVIFDHFSEKDYQRMLDLNRD 743
Db 766 NNAFQAQSGSALAQLYGT--SATLEHHFHFNAVMILQSEGHNFANLSKEYSDLMQLLKQ 824
Qy 744 IILATDLAHLRIPKDLQKMAEVG-YDRTNKQHRHSLLLCLLMTSCDLSDDQTKGWKTKRKI 802
Db 825 SILATDLTLFPERTEFFELVSKGEYDWNKYNHRDIFRSMMLTACDLGAVTKPWEISQV 884
Qy 803 AELIYKEFFSQGDLEK-AMGNRPMEMMDR-EKAYIPELQISFMHBIAMPIYKLLQDLFPK 860
Db 885 AELVTSEFFEQDRERLEKLTPSAIFDRNRKDELPRQLQLEWDSICMPLQALVKVNVK 944
Qy 861 AAEIYERVASNRHWTKVSHKFTIRGLPSNNS 892
Db 945 LKPLMDSVATNRSKWEELHQRLLASTASSSS 976

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Q95TW8 PRELIMINARY; PRT; 1018 AA.
ID Q95TW8
AC Q95TW8;
DT 01-DEC-2001 (TrEMBLrel. 19, Created)
DT 01-DEC-2001 (TrEMBLrel. 19, Last sequence update)
DT 01-MAR-2004 (TrEMBLrel. 26, Last annotation update)
DE GH27433p.
GN Name=Pde6; Synonyms=CG8279;
OS Drosophila melanogaster (Fruit fly).
OC Eukaryota; Metazoa; Arthropoda; Hexapoda; Insecta; Pterygota;
OC Neoptera; Endopterygota; Diptera; Brachycera; Muscomorpha;
OC Ephydroidea; Drosophilidae; Drosophila.
OX NCBI_TaxID=7227;
RN [1]
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RC STRAIN=Berkeley.
RA Stapleton M., Brokstein P., Hong L., Agbayani A., Carlson J.,
RA Champe M., Chavez C., Dorsett V., Farfan D., Frise E., George R.,
RA Gonzalez M., Guarin H., Li P., Liao G., Miranda A., Mungall C.J.,
RA Nunoo J., Pacile J., Paragas V., Park S., Phouanavong S., Wan K.,
RA Yu C., Lewis S.E., Rubin G.M., Celniker S.;
RA Submitted (OCT-2001) to the EMBL/GenBank/DBJ databases.
RL EMBL; AY058470; AAL13699.1; -.
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RL Genome Biol. 3:RESEARCH0079-RESEARCH0079 (2002).
RN [3]
RP SEQUENCE FROM N.A.
RX MEDLINE=22426070; PubMed=12537573;
RA Kaminker J.S., Bergman C.M., Krommiller B., Carlson J., Svirskas R.,
RA Patel S., Fries E., Wheeler D.A., Lewis S.E., Rubin G.M.,
RA Ashburner M., Celisner S.E.;
RT "The transposable elements of the Drosophila melanogaster euchromatin:
RT a genomics perspective.";
RL Genome Biol. 3:RESEARCH0084-RESEARCH0084 (2002).
RN [4]
RP SEQUENCE FROM N.A.
RX MEDLINE=22426069; PubMed=12537572;
RA Misra S., Crosby M.A., Mungall C.J., Matthews B.B., Campbell K.S.,
RA Hradecky P., Huang Y., Kaminker J.S., Millburn G.H., Prochuk S.E.,
RA Smith C.D., Tupy J.L., Whitfield E.J., Bayraktaroglu L., Berman S.P.,
RA Bettencourt B.R., Celisner S.E., de Grey A.D., Drysdale R.A.,
RA Harris N.L., Richter J., Russo S., Schroeder A.J., Shu S.Q.,
RA Stapleton M., Yamada C., Ashburner M., Gelbart W.M., Rubin G.M.,
RA Lewis S.E.;
RT "Annotation of the Drosophila melanogaster euchromatic genome: a
RT systematic review.";
RL Genome Biol. 3:RESEARCH0083-RESEARCH0083 (2002).
RN [5]
RP SEQUENCE FROM N.A.
RX SEQUENCE (SRP-2002) to the EMBL/GenBank/DBJ databases.
RL FlyBase;
RN Submitted (SRP-2002) to the EMBL/GenBank/DBJ databases.
RP FlyBase;
RX SEQUENCE FROM N.A.
RL Submitted (MAR-2004) to the EMBL/GenBank/DBJ databases.
RN EMBL; AB003705; AAF5066.3; -.
DR FlyBase; FBgn0038237; F066.
DR GO; GO:0004114; F:3',5'-cyclic-nucleotide phosphodiesterase a. . .; IEA.
DR GO; GO:0003824; F:catalytic activity; IEA.
DR GO; GO:0007165; P:signal transduction; IEA.
DR InterPro; IPR003018; GAF.
DR InterPro; IPR003607; Met_phos_hydro.
DR InterPro; IPR002073; PDEase.
DR Pfam; PF01590; GAF; 2.
DR PRINTS; PR00387; PDIESTERASE1.
DR SMART; SM00065; GAF; 2.
DR SMART; SM00471; HDG; 1.
DR PROSITE; PS00126; PDEASE_I; 1.
SQ SEQUENCE 1131 AA; 125638 MW; E63183B04B5FF08A CRC64;

Query Match
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Matches 264; Conservative 150; Mismatches 327; Indels 126; Gaps 24;

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DB |:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|
171 EKW---LTERAPPEALSRLQEFIEKRPKPSVTSLSLFCQWMAASPTVQOKSPRSLSNS 227
QY 206 DRKILQLC-----GELY-----DLDASSLQKVLQVLOQETQASRCLLIV- 246
DB |:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|
228 SASSLPECCRHLMDLDEGELFMELIRDVANELDIDLCHKILVNVGLLTHADRGSFLAK 287
QY 247 -SEDNLQSLCKV-----IGDKVLE---BEISPLTGTGLGVVEDKSKIQLKDLTSE 294
DB |:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|
288 GTPNKYLVAKLFDVYQTALKADVTRASAEIIPFGIGTAGVVAQTKOMINKEAYKD 347
QY 295 DMQQLQSMGLGEV-----QAMLCVPIGRATDQVVALACAFNKLGGDL-FTDQDBHV 345
DB |:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|
348 -----ARFNCIEIDLKTKYKTNAILCMBICNVEGD-IIGVAAIINKTNGCMFEHDHVEI 400
QY 346 IQCHFYTSTVLSTLAKQKQKLKCEQALQVAKNLFTHLDDVSVLLQELIIFEARNIS 405
DB |:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|
401 FRVYLTFCGIGIQNAQLFEMSVOEYRRNQIILNTARSIFESQNNLECLVTIMTEARELL 460
QY 406 NAEICSVFLLQON-----ELVAKV 424
DB |:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|
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RA Harris N.L., Harvey D., Heiman T.J., Hernandez J.R., Houck J.,  
RA Hostin D., Houston K.A., Howland T.J., Wei M.H., Ibegwam C.,  
RA Jalali M., Kalush F., Karpen G.H., Ke Z., Kennison J.A., Ketchum K.A.,  
RA Kimmel B.E., Kodira C.D., Kraft C., Kravitz S., Kulp D., Lai Z.,  
RA Laeko P., Lei Y., Levitsky A.A., Li J., Li Z., Liang Y., Lin X.,  
RA Liu X., Mattei B., McIntosh T.C., McLeod M.P., McPherson D.,  
RA Merkulov G., Milehina N.V., Mobarry C., Morris J., Moshrefi A.,  
RA Mount S.M., Moy M., Murphy B., Murphy L., Muzny D.M., Nelson D.L.,  
RA Nelson D.R., Nelson K.A., Nixon K., Nusskern D.R., Pacleb J.M.,  
RA Palazzolo M., Pittman G.S., Pan S., Pollard J., Puri V., Reese M.G.,  
RA Reinert K., Remington K., Saunders R.D., Scheeler F., Shen H.,  
RA Shue B.C., Siden-Kiamos I., Simpson M., Skupski M.P., Smith T.,  
RA Spier E., Spradling A.C., Stapleton M., Strong R., Sun E.,  
RA Svirskas R., Tector C., Turner R., Venter E., Wang A.H., Wang X.,  
RA Wang Z.Y., Wasarman D.A., Weinstein G.M., Weissbach J.,  
RA Williams S.M., Woodager, Worley K.C., Wu D., Yang S., Yao Q.A., Ye J.,  
RA Yeh R.F., Zaveri J.S., Zhan M., Zhang G., Zhao Q., Zheng L.,  
RA Zheng X.H., Zhong F.N., Zhong W., Zhou X., Zhu S., Zhu X., Smith H.O.,  
RA Gibbs R.A., Myers E.W., Rubin G.M., Venter J.C.,  
RT "The genome sequence of *Drosophila melanogaster*;"  
RL Science 287:2185-2195(2000).  
RN [2]  
RP SEQUENCE FROM N.A.  
EX MEDLINE-22426065; PubMed-12537568;  
RA Celnikier S.E., Wheeler D.A., Kronmiller B., Carlson J.W., Halpern A.,  
RA Patel S., Adams M., Champe M., Dugan S.P., Frise E., Hodgson A.,  
RA George R.A., Hoskins R.A., Laverty T., Muzny D.M., Nelson C.R.,  
RA Pacleb J.M., Park S., Pfeiffer B.D., Richards S., Sodergren E.J.,  
RA Svirskas R., Tabor P.E., Wan K., Stapleton M., Sutton G.G., Venter C.,  
RA Weinstein G., Scherer S.E., Myers E.W., Gibbs R.A., Rubin G.M.,  
RT "Finishing a whole-genome shotgun: Release 3 of the *Drosophila*  
RT melanogaster euchromatic genome sequence."  
RL Genome Biol. 3:RESEARCH0079-RESEARCH0079(2002).  
RN [3]  
RP SEQUENCE FROM N.A.  
EX MEDLINE-22426070; PubMed-12537573;  
RA Kaminker J.S., Bergman C.M., Kronmiller B., Carlson J., Svirskas R.,  
RA Patel S., Frise E., Wheeler D.A., Lewis S.E., Rubin G.M.,  
RA Ashburner M., Celnikier S.E.,  
RT "The transposable elements of the *Drosophila melanogaster* euchromatin:  
RT a genomics perspective."  
RL Genome Biol. 3:RESEARCH0084-RESEARCH0084(2002).  
RN [4]  
RP SEQUENCE FROM N.A.  
EX MEDLINE-22426069; PubMed-12537572;  
RA Misra S., Crosby M.A., Mungall C.J., Matthews B.B., Campbell K.S.,  
RA Hradecky P., Huang Y., Kaminker J.S., Millburn G.H., Prochnik S.E.,  
RA Smith C.D., Tupy J.L., Whitfield E.J., Bayraktaroglu L., Berman B.P.,  
RA Bettencourt B.R., Celnikier S.E., de Grey A.D., Drysdale R.A.,  
RA Harris N.L., Richter J., Russo S., Schroeder A.J., Shu S.O.,  
RA Stapleton M., Yamada C., Ashburner M., Gelbart W.M., Rubin G.M.,  
RA Lewis S.E.,  
RT "Annotation of the *Drosophila melanogaster* euchromatic genome: a  
RT systematic review."  
RL Genome Biol. 3:RESEARCH0083-RESEARCH0083(2002).  
RN [5]  
RP SEQUENCE FROM N.A.  
EX SEQUENCE (SEP-2002) to the EMBL/GenBank/DBJ databases.  
RL FlyBase;  
RN Submitted (MAR-2004) to the EMBL/GenBank/DBJ databases.  
RL EMBL: AE003659; AAF3675.2; -;  
DR FlyBase; FBgn0032686; Pdel1.  
DR GO: GO:000414; F:3,5'-cyclic-nucleotide phosphodiesterase a. . .; IEA.  
DR GO: GO:0003824; F:catalytic activity; IEA.  
DR GO: GO:0007165; F:signal transduction; IEA.  
DR InterPro; IPR003018; GAF.  
DR InterPro; IPR003607; Met\_phos\_hydro.  
DR InterPro; IPR002073; PDEase.  
DR Pfam; PF01590; GAF; 2.  
DR Pfam; PF00233; PDEase\_1; 1.

DR PRINTS; PR00387; PD1ESTERASE1.  
DR SMART; SM00065; GAF; 2.  
DR SMART; SM00471; HGC; 1.  
DR PROSITE; PS00126; PDEase I; 1.  
SQ SEQUENCE 1365 AA; 151175 MW; B0562E2FDF5012E56 CRC64;  
Query Match 20.6%; Score 983; DB 2; Length 1365;  
Best Local Similarity 31.3%; Pred. No. 4.1e-50;  
Matches 246; Conservative 147; Mismatches 303; Indels 90; Gaps 19;  
QY 209 ILQCGELYDLIDASSLQLKVLQYLOQETOASRCCLLV-----SEDLQLSCKV----- 257  
DB 299 VKDINCNE---LEVRTLCHKILQNVISILLNADRGSFLVQGRGNGPGLK-KCLVSKLFDV 354  
QY 258 -----IGDKVLEEISFPPLTTRGLRGQVVEDKKSIOQLKDLTSDM--QQQLSMGLGCVQAM 310  
DB 355 CPRSTVEEMEQQDEVRAVWGVTGIAGHVAESGEPVNPIDAYQDERFNCIEDLSLTGYRTKAL 414  
QY 311 LCVPIVSIRATDOVALACAFNKLGGDLFTDQDEHVIOHCFHYTSTVLTSTLAFQKEOKLK 370  
DB 415 LCMPIKDSGD-VIGVAQVINNMNGECFSEIDKRVFSSYLPQCGIGLRNAQLYKESQLEI 473  
QY 371 CECQALLOVAKNLFTHLDDVSVLLQEIITEARNLSNAEICSVELLDONE--LVAKVFD-- 426  
DB 474 KKNQVLLDLARMIFFEEQSTIEHNVPRILTHMQSLQCQVQVLLVHEADKGSFVRVDFE 533  
QY 427 -GGVVEDES-----YEIRPADQGIAGHVATTGQILNIPDAYAHPLFYRGVDDSTGFR 479  
DB 534 ANDLSEERATSRSTPESRFPINIGITGHVATTGETVNVPNAYEDDRFDASVDENSCPKH 593  
QY 480 RNILCFPTINENQEVIGVAELVNKINGPWFSEFDELATAPFSIYCGISIAHLLYKKNVE 539  
DB 594 RSILCMAIKNSLGQIIGVIQILNKFNELDFTKNDENFVEAFAPFCMGHINHTMYEKATV 653  
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DB 654 AMAQSVTLVLSYHASATMDENRHRKQKQQAQVGLRQAPLSPPRKKLQRLRVP 713  
QY 576 IDSINPASYTPRSIPEDDTSMAILSMLQDMFNINNYKIDCPTLARFCLMVKVGYRDP 635  
DB 714 VHFRLHDFKDDIHFEDDDTLKACLRMFLDLDVFERPHIDYELVLCRWLLSVKKNYRNV 773  
QY 636 HNWMAFVSVSHFCYLLYKNLELTNYLEDMEFALFISCHDLDHRGTNNSFQVASKVL 695  
DB 774 HNWRAFNVAQWMAFALTITQWKKIFGIECLALIIGCLCHDLDRGTNNSFQIKASSPL 833  
QY 696 AALYSSEGSVMERHFAQAIILNTHGNIIDPHERKDYQYRMLDMLDRDIILATDLAHLR 755  
DB 834 AOLYST--STWEHHFDCQLMILNSPGNQLANLSSDDYCRVIRVLEDDAILSTDLAVY-- 889  
QY 756 IFKD----LQMAEYGYDRTNKHSHLLCLLMTSCDLSDDQTKGKWTTRKIAELIYKEFF 911  
DB 890 -FKKGGPFLSVSQPTSVMVAEPEPALLRAMSMTVCDLSAITKWEIKRVADLVSEFF 948  
QY 812 SQGDLEKAMGN-RPMEMMDREKA-YIPELOISFMEHIAMPIYKLLQDLFPKAAELYVERVA 869  
DB 949 EQGOMEKQELNITPIDINREKEDELPMQVNFIDISICLPIYEAFTLSKLEPLVEGVR 1008  
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AC Q8VID6;  
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DT 01-MAR-2002 (TrEMBLrel. 20, Last sequence update)

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DT 01-MAR-2004 (Tremblrel. 26, Last annotation update)
DE Phosphodiesterase 11A4.
GN Name=RNPD11A4;
OS Rattus norvegicus (Rat).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Rattus.
OX NCBI_taxID=10116;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=2139348; PubMed=11502204;
RA Yuasa K., Ohgura T., Aashina M., Omori K.;
RT "Identification of rat cyclic nucleotide phosphodiesterase 11A
RT (PDE11A): comparison of rat and human PDE11A splicing variants.";
RL Euk. J. Biochem. 268:4440-4448(2001).
DR EMBL; AB059362; BAB79629.1; -.
DR GO; GO:0004114; F:3',5'-cyclic-nucleotide phosphodiesterase a. . .; IEA.
DR GO; GO:0003824; F:catalytic activity; IEA.
DR GO; GO:0007165; F:signal transduction; IEA.
DR Pfam; PF01590; GAF; 2.
DR Pfam; PF00233; PDEase_I; 1.
DR PRINTS; PRO0387; PDIESTERASE1.
DR SMART; SM00065; GAF; 2.
DR SMART; SM00471; HDC; 1.
DR PROSITE; PS00126; PDEASE_I; 1.
DR PROSITE; PS00126; PDEASE_I; 1.
SQ SEQUENCE 935 AA; 104570 MW; E80F103970F8276 CRC64;

Query Match 20.5%; Score 979; DB 2; Length 935;
Best Local Similarity 30.9%; Pred. No. 4.1e-50;
Matches 248; Conservative 157; Mismatches 312; Indels 86; Gaps 20;

Qy 143 VHCGLSDNEWSLQAVEKHTLVAKRVQALQOQRESSVAP-----EATONPPE-- 190
Db 131 IHVNTYD-EQVTSRAQPLSSV---RRALLRKASSLPPTAHILSALLESRVNLQYPP 186

Qy 191 BAAGDQKGGVAYTNQDRKIQLCGEL-YDLDASSLQLKVLQYLOQETOASRCCLLLYSED 249
Db 187 PTAIDYKCHLKXKNERQFLESLVXDINDLDLTSLYKILIPVCLMVDADRCSLFLV--E 244

Qy 250 NLQLSCKVIGDKVLE-----EETSPPLTTGRLGQGVVEDKKSIOIKDLTS 293
Db 245 GAAAGKKTLSKFFDFVHAGTPLLPGCTTENSNEVQVPMWGKIIGYVGEHGETVNIQAYQ 304

Qy 294 EDM--QQLSQMLGCVQVAMLCVPVSRATDOVALACAFNKL-GGDLFTDODEHVIOHCF 350
Db 305 DRRNDEIDKUTGYTKSLLCMP-IRNSDGEIIGVAQINKVPEGAPTEDEKVMQNYL 363

Qy 351 HYTSVTLTSLAFQKEQKCEQALQVAKNLFTHLDDVSVLLQBIITEARNLSNABIC 410
Db 364 PFCGTAISNAQLFAASRKEYERSRALLEVNDLFEEQTDLEKIVKKIMHRAQTLLKCERC 423

Qy 411 SVFLLDQNELVAKVPDGGVVEDESYEIRIP-----ADQGIAG 447
Db 424 SVLLLEDIESPVKVF-----TKSFELMSPKCSADAENSFKESVKSYSWDLINNSTAE 477

Qy 448 HVATTGQILNIPDAYHPLFYRGVDDSTGRTRNLCPPIKNEOEVIGVAELVKNKNGP 507
Db 478 LVASTGLPVPVSDAYQDPRFAEADQISGFHRSVLCVPIWNSHQIIGVAVQLNRLLDGK 537

Qy 508 WFSKFDDELATAFSTCYGISIAHSLLYKKNVNAQYRSHLANEMMMYHKVSDDEYTKLLH 567
Db 538 PFDDADQRLFEAFVIFCGLGINNTIMYDQVKKSWAKQSVALLDVLSTHATCSKAEDVKFKA 597

Qy 568 DGIQPVAAI----DSNFASFTYTPRSLPEDDTSMAILSMLQDMNFNNYKIDCPTLARFCL 624
Db 598 ANIPLVSELAIDDIHFDDF-----SLDVDAMITTAALRMFMELGMVQKFKIDYETLCRWLL 652

Qy 625 MVKGGYRDPYPVNMWHPVSVSHFCVLLYKLELNTY---LEDMEIFALFISCMCHDLDDR 681
Db 653 TVRKNRMVLYHNWRHAFNV---COLMPAMLTAGFQELTEVELAVIVGLCHDLDDR 709

Qy 682 GTNNSFQVAKSVLAALYSSEGSVNERHHFAQAIATLNTGCHNIPDFHSRKYQRMULDLM 741
Db 710 GTNNAFOAKSDSALAQLYGT-SATLEHHFHFHNAVMILOQSEGHNIPANLSKEYSDLMQLL 768
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Qy 742 RDIILATDLAHLRIIPKDLQKMAEVG-YDRTNKOHHSLLCLLMTSCDLSQTKGWKTR 800
Db 769 QKSILATDLYFERRTEFFELVSKGAYDWSITSHRDVFRRSMLMTACDLGAVTKPWEISR 828
Qy 801 KIAELIYKEPFSQGDLEKA-MGNRPMMEMDR-EKAYIPELQISFMEHIAMPIYKLLQDLF 858
Db 829 QVAELVTSEFFEQGDRESESLKLTSPSAIFDENRRKDELPRLOLEWIDSICMPLYQALVKVN 888
Qy 859 PKAAELYERVASNRHHTKVS HK 881
Db 889 AKLKPMLDSVAANRRKWEELHOK 911
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Search completed: June 26, 2005, 12:21:45  
Job time : 134.535 secs

GenCore version 5.1.6  
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OM protein - protein search, using sw model

Run on: June 26, 2005, 12:09:51 ; Search time 31.6393 Seconds  
(without alignments)  
2800.810 Million cell updates/sec

Title: US-10-697-894-39  
Perfect score: 4781  
Sequence: 1 MRRQPAASRDLPFAQFVPPG.....VPLDGLARAPINGCCSLDAE 921  
Scoring table: BLOSUM62  
Gapop 10.0 , Gapext 0.5

Searched: 283416 seqs, 96216763 residues  
Total number of hits satisfying chosen parameters: 283416

Minimum DB seq length: 0  
Maximum DB seq length: 2000000000  
Post-processing: Minimum Match 0%  
Maximum Match 100%  
Listing first 45 summaries

Database : PIR 79:.\*  
1: pir1.\*  
2: pir2.\*  
3: pir3.\*  
4: pir4.\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	4781	100.0	921	1 A40981	3',5'-cyclic-nucle
2	4324.5	90.5	928	1 JC2486	3',5'-cyclic-nucle
3	938.5	19.6	918	2 D85544	protein R08D7.6 [i
4	938	19.6	841	1 S24462	probable 3',5'-cyc
5	819.5	17.1	854	2 A42828	3',5'-cyclic-GMP p
6	801	16.8	875	1 JW0106	3',5'-cyclic-GMP p
7	799.5	16.7	853	2 A36617	3',5'-cyclic-GMP p
8	799.5	16.7	862	2 I50186	3',5'-cyclic-GMP p
9	799	16.7	856	1 A47451	3',5'-cyclic-GMP p
10	791	16.5	856	2 S30762	3',5'-cyclic-GMP p
11	789	16.5	875	1 A48719	3',5'-cyclic-GMP p
12	786	16.4	855	2 A43810	3',5'-cyclic-GMP p
13	758.5	15.9	858	2 JC4520	3',5'-cyclic-GMP p
14	756	15.8	800	2 S13032	3',5'-cyclic-GMP p
15	754.5	15.8	859	1 S08418	3',5'-cyclic-GMP p
16	741.5	15.2	859	2 S13030	3',5'-cyclic-GMP p
17	726	15.2	859	2 B34611	3',5'-cyclic-GMP p
18	696	14.6	393	2 T25590	hypothetical prote
19	404	8.5	859	2 AC2089	adenylate cyclase
20	390.5	8.2	664	2 T24459	hypothetical prote
21	383.5	8.0	712	2 S71626	3',5'-cyclic-nucle
22	382.5	8.0	673	2 I61358	3',5'-cyclic-nucle
23	381.5	8.0	549	2 T16769	hypothetical prote
24	380.5	8.0	584	2 B53109	3',5'-cyclic-nucle
25	380.5	8.0	672	2 I61259	3',5'-cyclic-nucle
26	380.5	8.0	886	2 A54442	3',5'-cyclic-nucle
27	379.5	7.9	536	2 I67945	3',5'-cyclic-nucle
28	379	7.9	562	2 I59143	CAMP phosphodiester
29	379	7.9	564	2 A40949	cyclic-AMP phospho

30	375	7.8	610	2 I67946	3',5'-cyclic-nucle
31	375	7.8	844	2 I53865	phosphodiesterase
32	374	7.8	564	2 JC1519	3',5'-cyclic-nucle
33	374	7.8	736	2 I61354	phosphodiesterase
34	363.5	7.6	777	2 S65543	3',5'-cyclic-nucle
35	350	7.3	519	2 T14783	hypothetical prote
36	345.5	7.2	534	1 A44162	3',5'-cyclic-nucle
37	343.5	7.2	535	1 A46378	3',5'-cyclic-nucle
38	341.5	7.1	535	1 A44161	3',5'-cyclic-nucle
39	341	7.1	530	1 A45334	3',5'-cyclic-nucle
40	340	7.1	768	2 T10796	3',5'-cyclic-nucle
41	335.5	7.0	536	1 JC5129	3',5'-cyclic-nucle
42	329	6.9	267	2 B33904	CAMP phosphodiester
43	328.5	6.9	860	2 AB2044	adenylate cyclase
44	327	6.8	498	2 A47286	3',5'-cyclic-AMP p
45	325.5	6.8	323	2 S55348	3',5'-cyclic-nucle

ALIGNMENTS

RESULT 1

A40981  
3',5'-cyclic-nucleotide phosphodiesterase (EC 3.1.4.17), cGMP-stimulated - bovine  
N:Alternate names: cGMP-dependent phosphodiesterase  
C:Species: Bos primigenius taurus (cattle)  
C:Date: 26-Aug-1999 #sequence revision 26-Aug-1999 #text change 09-Jul-2004  
C:Accession: A40981; B36112; A36112; B26650; A60179; C26650  
R:Sonnenburg, W.K.; Mullaney, P.J.; Beavo, J.A.  
J. Biol. Chem. 266, 17655-17661, 1991  
A:Title: Molecular cloning of a cyclic GMP-stimulated cyclic nucleotide phosphodiesterase  
A:Reference number: A40981; MUID:91373395; PMID:1654333  
A:Accession: A40981  
A:Molecule type: mRNA  
A:Residues: 1-921 <SON>  
A:Cross-references: UNIPROT:P14099; GB:M73512; NID:g162829; PIDN:AAA74559.1; PID:g162831  
R:Le Trong, H.; Beier, N.; Sonnenburg, W.K.; Stroop, S.D.; Walsh, K.A.; Beavo, J.A.; Ch  
Biochemistry 29, 10280-10288, 1990  
A:Title: Amino acid sequence of the cyclic GMP-stimulated cyclic nucleotide phosphodiesterase  
A:Reference number: A36112; MUID:91104948; PMID:2176866  
A:Accession: B36112  
A:Status: not compared with conceptual translation  
A:Molecule type: mRNA  
A:Residues: 592-921 <LET>  
A:Accession: A36112  
A:Molecule type: protein  
A:Residues: 1-203, 'D', 205-477, 'Q', 479-921 <LET2>  
R:Charbonneau, H.; Beier, N.; Walsh, K.A.; Beavo, J.A.  
Proc. Natl. Acad. Sci. U.S.A. 83, 9308-9312, 1986  
A:Title: Identification of a conserved domain among cyclic nucleotide phosphodiesterase  
A:Reference number: A26650; MUID:87092242; PMID:3025833  
A:Accession: B26650  
A:Molecule type: protein  
A:Residues: 613-632, 'L', 634-794, 808-868 <CHA>  
R:Experimental source: heart  
R:Tanaka, T.; Hockman, S.; Moos Jr., M.; Taira, M.; Meacci, E.; Murashima, S.; Manganiello  
Second Messengers Phosphoproteins 13, 87-98, 1991  
A:Title: Comparison of putative cGMP-binding regions in bovine brain and cardiac cGMP-s  
A:Reference number: A60179; MUID:92065414; PMID:1659635  
A:Accession: A60179  
A:Status: not compared with conceptual translation  
A:Molecule type: mRNA  
A:Residues: 311-803, 'DV', 806-921 <TAN>  
A:Note: part of this sequence was confirmed by protein sequencing  
C:Superfamily: 3',5'-cyclic-nucleotide phosphodiesterase, cGMP-stimulated; 3',5'-cyclic  
C:Keywords: acetylated amino end; alternative splicing; CAMP binding; cGMP binding; hom  
F:635-857/Domain: 3',5'-cyclic-nucleotide phosphodiesterase homology <CNPD>  
F:1/Modified site: acetylated amino end (Met) #status experimental

Query Match 100.0%; Score 4781; DB 1; Length 921;  
Best Local Similarity 100.0%; Pred. No. 2e-304;  
Matches 921; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 MRRQPAASRDLPFAQRPVPPGSDGALQDALLSLGSDVIDVAGLQQAQVKEALSIVLPKVETV 60  
Db 1 MRRQPAASRDLPFAQRPVPPGSDGALQDALLSLGSDVIDVAGLQQAQVKEALSIVLPKVETV 60  
QY 61 YTYLLDGSRLVCEPPELPOEGKVRBAVISRKELGCGNGLGPSDLPKPKPLARLVAPLAP 120  
Db 61 YTYLLDGSRLVCEPPELPOEGKVRBAVISRKELGCGNGLGPSDLPKPKPLARLVAPLAP 120  
QY 121 DTQVLVILPLVKEAGAAVAILVHCGQLSDNEEWSLQAVEKHTLVALKRVQALQORESSV 180  
Db 121 DTQVLVILPLVKEAGAAVAILVHCGQLSDNEEWSLQAVEKHTLVALKRVQALQORESSV 180  
QY 181 APEATONPEEAAGDQKGGVATYNODRKILQCGELYDLDAASSLQKLVQVLOQETQASR 240  
Db 181 APEATONPEEAAGDQKGGVATYNODRKILQCGELYDLDAASSLQKLVQVLOQETQASR 240  
QY 241 CCLLLVSDNQLQSCKVIGDKVLEEEISFPPLTTGRLGQVVEDKKSQIQKDLTSEDMDQQLQ 300  
Db 241 CCLLLVSDNQLQSCKVIGDKVLEEEISFPPLTTGRLGQVVEDKKSQIQKDLTSEDMDQQLQ 300  
QY 301 SMLGCEVQAMLCVVISRATQVVALACAFNKLGGDLFTDQDEHVIQCHFYTSTVLST 360  
Db 301 SMLGCEVQAMLCVVISRATQVVALACAFNKLGGDLFTDQDEHVIQCHFYTSTVLST 360  
QY 361 LAFQKEQKLKCEQALLQVAKNLFTHLDVSVLQEIITEARNLSNAEICSVFLLDQNEL 420  
Db 361 LAFQKEQKLKCEQALLQVAKNLFTHLDVSVLQEIITEARNLSNAEICSVFLLDQNEL 420  
QY 421 VAKVPDGGVVEDESVEIRIPADQGIAGHVATTGQILNIPDAYAHPLFYRGVDDSTGFRTR 480  
Db 421 VAKVPDGGVVEDESVEIRIPADQGIAGHVATTGQILNIPDAYAHPLFYRGVDDSTGFRTR 480  
QY 481 NILCPPIKNEQEVIGVAELVNKINGPWFSPKDEDLATAFSIYCGISIAHSLLYKKVNEA 540  
Db 481 NILCPPIKNEQEVIGVAELVNKINGPWFSPKDEDLATAFSIYCGISIAHSLLYKKVNEA 540  
QY 541 QYRSHLANEMMYHMKVSDDEVTKLLHDGIQPVAIDSNFASFTYTPRSLPEDDTSMAIL 600  
Db 541 QYRSHLANEMMYHMKVSDDEVTKLLHDGIQPVAIDSNFASFTYTPRSLPEDDTSMAIL 600  
QY 601 SMLQDMFNINNYKIDCPTLARFCLMVKKGYRDPYPYHNMWHAFSVSHFCYLLYKXLELNY 660  
Db 601 SMLQDMFNINNYKIDCPTLARFCLMVKKGYRDPYPYHNMWHAFSVSHFCYLLYKXLELNY 660  
QY 661 LEDMEIFALFISCMCHDLDRGTNNSFQVASKSVLAALYSSEGSVMERHHPFAQAIILNT 720  
Db 661 LEDMEIFALFISCMCHDLDRGTNNSFQVASKSVLAALYSSEGSVMERHHPFAQAIILNT 720  
QY 721 HGCNIFDHFSRKDYQYRMLDLMRDIIILATDLAHLRIFKDLQKMAEVGYDRNKHHSLLL 780  
Db 721 HGCNIFDHFSRKDYQYRMLDLMRDIIILATDLAHLRIFKDLQKMAEVGYDRNKHHSLLL 780  
QY 781 CLMTSCDLSQDTQKWKTRKIAELIYKEFFSQGDEKAMGNRPMEMMDREKAYIPELOI 840  
Db 781 CLMTSCDLSQDTQKWKTRKIAELIYKEFFSQGDEKAMGNRPMEMMDREKAYIPELOI 840  
QY 841 SFMEHIAMPIYKLLQDLFPKAAELYERVASNREHWTKVSHKFTIRGLPSNNSLDFLDEY 900  
Db 841 SFMEHIAMPIYKLLQDLFPKAAELYERVASNREHWTKVSHKFTIRGLPSNNSLDFLDEY 900  
QY 901 EVPDLGARAINGCCSLDAE 921  
Db 901 EVPDLGARAINGCCSLDAE 921

RESULT 2  
JC2486  
3',5'-cyclic-nucleotide phosphodiesterase (EC 3.1.4.17), cGMP-stimulated - rat  
N:Alternate names: cGMP-dependent phosphodiesterase  
C:Species: Rattus norvegicus (Norway rat)  
C:Date: 26-Aug-1999 #sequence\_revision 26-Aug-1999 #text\_change 09-Jul-2004  
C:Accession: JC2486

R;Yang, Q.; Paikind, M.; Bolger, G.; Thompson, W.J.; Repaske, D.R.; Cutler, L.S.; Epstein Biochem. Biophys. Res. Commun. 205, 1850-1858, 1994  
A:Title: A novel cyclic GMP stimulated phosphodiesterase from rat brain.  
A:Reference number: JC2486; MUID:95110334; PMID:7811274  
A:Accession: JC2486  
A:Molecule type: mRNA  
A:Residues: 1-928 <YAN>  
A:Cross-references: UNIPROT\_Q01062; GB:U21101; NID:g706929; PIDN:AAA63683.1; PID:g706930  
A:Experimental source: brain  
C:Superfamily: 3',5'-cyclic-nucleotide phosphodiesterase, cGMP-stimulated; 3',5'-cyclic-nucleotide phosphodiesterase, cAMP binding; homodimer; phosphoprotein;  
C:Keywords: alternative splicing; cAMP binding; homodimer; phosphoprotein;  
P:643-865/Domain: 3',5'-cyclic-nucleotide phosphodiesterase homology <CNPD>  
P:109/Binding site: phosphate (Ser) (covalent) (by protein kinase A) #status predicted

Query Match 90.5%; Score 4324.5; DB 1; Length 928;  
Best Local Similarity 91.7%; Pred. No. 1.4e-274;  
Matches 830; Conservative 32; Mismatches 38; Indels 5; Gaps 2;

QY 15 EPVPPGSDGALQDALLSLGSDVIDVAGLQQAQVKEALSIVLPKVETVYTYLLDGSRLVCE 74  
Db 28 EPPQPCAD-SLQDALLSLGAVIDIAGLQQAQVKEALSIVLPKVETVYTYLLDGSRLVCE 86  
QY 75 EPPHELPOEGKVRBAVISRKELGCGNGLGPSDLPKPKPLARLVAPLAPDTQVLVILPLVKEA 134  
Db 87 DPPHELPOEGKVRBAVISRKELGCGNGLGPSDLPKPKPLARLVAPLAPDTQVLVILPLVKEA 146  
QY 135 GAVAAVILVHCGQLSDNEEWSLQAVEKHTLVALKRVQALQORESSVAPATONPEEAAG 194  
Db 147 GTVAAVILVHCGQLSDNEEWSLQAVEKHTLVALKRVQALQORESSVAPATONPEEAAG 202  
QY 195 DQKGGVATYNODRKILQCGELYDLDAASSLQKLVQVLOQETQASRCLLLVSDNQLQ 254  
Db 203 DQKDEKGYTAHDKILQCGELYDLDAASSLQKLVQVLOQETQATHCCLLLVSDNQLQ 262  
QY 255 CKVIGDKVLEEEISFPPLTTGRLGQVVEDKKSQIQKDLTSEDMDQQLQSMGCEVQAMLCVP 314  
Db 263 CKVIGDKVLEEEISFPPLTTGRLGQVVEDKKSQIQKDLTSEDMDQQLQSMGCEVQAMLCVP 322  
QY 315 VISRATQVVALACAFNKLGGDLFTDQDEHVIQCHFYTSTVLSTLAFQKEQKLKCEQ 374  
Db 323 VISRATQVVALACAFNKLGGDLFTDQDEHVIQCHFYTSTVLSTLAFQKEQKLKCEQ 382  
QY 375 ALLQVAKNLFTHLDVSVLQEIITEARNLSNAEICSVFLLDQNELVAKVPDGGVVEDES 434  
Db 383 ALLQVAKNLFTHLDVSVLQEIITEARNLSNAEICSVFLLDQNELVAKVPDGGVVEDES 442  
QY 435 YEIRIPADQGIAGHVATTGQILNIPDAYAHPLFYRGVDDSTGFRTRNILCPPIKNEQEV 494  
Db 443 YEIRIPADQGIAGHVATTGQILNIPDAYAHPLFYRGVDDSTGFRTRNILCPPIKNEQEV 502  
QY 495 IGVAELVNKINGPWFSPKDEDLATAFSIYCGISIAHSLLYKKVNEAQYRSHLANEMMYH 554  
Db 503 IGVAELVNKINGPWFSPKDEDLATAFSIYCGISIAHSLLYKKVNEAQYRSHLANEMMYH 562  
QY 555 MKVSDDEVTKLLHDGIQPVAIDSNFASFTYTPRSLPEDDTSMAILSMLQDMFNINNYKI 614  
Db 563 MKVSDDEVTKLLHDGIQPVAIDSNFANFTYTPRSLPEDDTSMAILSMLQDMFNINNYKI 622  
QY 615 DCPTLARFCLMVKKGYRDPYPYHNMWHAFSVSHFCYLLYKXLELNTLYLEDMEIFALFISCM 674  
Db 623 DCPTLARFCLMVKKGYRDPYPYHNMWHAFSVSHFCYLLYKXLELNTLYLEDMEIFALFISCM 682  
QY 675 CHDLDHRGTNNSFQVASKSVLAALYSSEGSVMERHHPFAQAIILNTHGCNIFDHFSRKDY 734  
Db 683 CHDLDHRGTNNSFQVASKSVLAALYSSEGSVMERHHPFAQAIILNTHGCNIFDHFSRKDY 742  
QY 735 QRMELDLMRDIIILATDLAHLRIFKDLQKMAEVGYDRNKHHSLLLCLMTSCDLSQDTQK 794  
Db 743 QRMELDLMRDIIILATDLAHLRIFKDLQKMAEVGYDRNKHHSLLLCLMTSCDLSQDTQK 802  
QY 795 GWKTRKIAELIYKEFFSQGDEKAMGNRPMEMMDREKAYIPELOISFMEHIAMPIYKLL 854  
Db 803 GWKTRKIAELIYKEFFSQGDEKAMGNRPMEMMDREKAYIPELOISFMEHIAMPIYKLL 862

QY 855 QDLFPPKAAELYERVASNRHHTWKVSHKFTIRGLPSSNLSLDFLDEEVEVPLDGCARAPING 914  
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Db 863 QDLFPPKAAELYERVASNRHHTWKVSHKFTIRGLPSSNLSLDFLDEEVEVPLDVTAPVNG 922  
|||||  
QY 915 CCSDL 919  
|||||  
Db 923 CCSL 927  
|||||  
RESULT 3  
D88544  
protein R08D7.6 [imported] - Caenorhabditis elegans  
C:Species: Caenorhabditis elegans  
C>Date: 10-May-2001 #sequence\_revision 10-May-2001 #text\_change 09-Jul-2004  
C:Accession: D88544  
R:anonymous, The C. elegans Sequencing Consortium.  
Science 282, 2012-2018, 1998  
A:Title: Genome sequence of the nematode C. elegans: a platform for investigating biolog  
A:Reference number: A75000; MUID:99069613; PMID:9851916  
A>Note: see website genome.wustl.edu/gac/C.elegans/ and www.sanger.ac.uk/Projects/C\_ele  
A>Note: published errata appeared in Science 283, 35, 1999; Science 283, 2103, 1999; and  
A:Accession: D88544  
A>Status: preliminary  
A:Molecule type: DNA  
A:Residues: 1-918 <STO>  
A:Cross-references: UNIPROT:P30645; GB:chr\_III; PIDN:CAA78052.1; PID:g3878939; GSPDB:GNO  
C:Genetics:  
A:Gene: R08D7.6  
A:Map position: 3  
C:Superfamily: Caenorhabditis probable 3',5'-cyclic-nucleotide phosphodiesterase R08D7.6  
Query Match 19.6%; Score 938.5; DB 2; Length 918;  
Best Local Similarity 30.3%; Pred. No. 3.6e-53;  
Matches 243; Conservative 135; Mismatches 281; Indels 143; Gaps 19;  
QY 146 GOLSNEEWSLQAVK-HTVLALKRVA-----LQORSSVAPEATQNP 189  
|||  
Db 18 GDEEEIEISENNKRRKLTLSAVALADIAYSQRIACSMLELRNRSPPSAHPSP 77  
|||  
QY 190 BEAGDQKG-GVAYTNQDKILQLC-----GELYDLASSLQLKV----- 228  
|||  
Db 78 TNCQNSQDGLHHHHEAASGTCGGMVTGTGANAASNEPAGSASPTVWRTSHPP 137  
|||  
QY 229 LOYLOQETOASRCCLLSLSEDNLQSKVIGDK-----VLEBEISFPITTTGRLGQVDEK 283  
|||  
Db 138 LHFNNNEIR-----NRNLQMLKRGTKDDWASLRVDIEPTSSGLL-ELLPD- 185  
|||  
QY 284 KSIQLKDLTSEDMDQLQSMGLGEVQAMLCVPVISRATQVVALACAFNKLGGDLFTDQDE 343  
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Db 186 -----VPIVKLSRPLVKM-----DQDD 204  
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QY 344 HVIOHCFHYTSTLSTLAFQEKQKCEQALLQVAKNLFTHLDDVSVLQEIITEARN 403  
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Db 205 ACSVASNESDRVTLSPLVPMISFDQFLC-----LTNNL-----SALISCIATAEAKK 250  
|||  
QY 404 LSNABICSVFLLDQ-----NE---LVAKVFDGQVVEDESYEIRIPADOGIAGHVAT 451  
|||  
Db 251 NTEADYAVFLHDEKNQVLFNNETMLTKGKFDWG-----YGIYGVKVAS 296  
|||  
QY 452 TQGLINIPDAYAHLFYRGVDSTGFRTRNLICFPKINENQVIGVAELVNKINGPWFPSK 511  
|||  
Db 297 TMTWNRIDVSRCPFFNEIDQFSIKARNLIAFLIDSSCSLIGVIVLYNKENG--FSR 354  
|||  
QY 512 FDELATAFSIVCGISIAHSLLYKKVNAQYSHLANEMMY--HMKVSDDDEYTKLLHDG 569  
|||  
Db 355 HDEKIKRFSYFVASIAHAIAKQIEVTRIHVMVEEFKIQGEDAVIEEVDIMRLVNDP 414  
|||  
QY 570 IQPVAADISNFSFTYTPRSLPEDDTSMALLSMDQMPINNYKIDCPTLAPFCLMWKKG 629  
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Db 415 LDWRYFQNFADFPFPRASVGENHFRASMMFFDLGFSMLYKLNKRLSLVLVRVAG 474  
|||  
QY 630 YRDPYHNHMAFSVSHFCYLLYKNLNTYLEDMEIFALFISCMCHDLHRGTNNSPQV 689  
|||

Db 475 YRPVYHNWSHAPVTHFCWLTLRDTARRALSDMERUSLLIACLCHDIDHRGTNSFQM 534  
|||||  
QY 690 AS--KSVLAALYSSEGSVMRHHFAQAIATLTHGNCNIPDFHSRKYQRMOLDLMDIILA 747  
|||  
Db 535 QSLQKTPLSVLSTEGSVLERHHFAQIKLQOECSILENLPADFRIVTIREVILA 594  
|||  
QY 748 TDLAHLRIFKDLQMAEVGYDRTNKQHHSLLLCLLMTSCDLSQDTGKWKTRKIAELIY 807  
|||  
Db 595 TDISALRKQERIKTMISEGVNPMSPDHRLLYLLMCLVMTASDLSQAKNPFNAKRIAENIY 654  
|||  
QY 808 KEFFSOGDLKAMGNRPMEMMDREKAYIPELQISMEHTAMPIYKLLQDLFPCAALYER 867  
|||  
Db 655 LEFFAQGDLLEQLGVKPLEMMDRTWAYVPTQIDFLKIGVVPFQLLASVPEGRTTSEA 714  
|||  
QY 868 VASNREHRTKVSHKFTIRGLPS 889  
|||  
Db 715 IDANHLCHVALDEE--VRNPS 734  
|||  
RESULT 4  
S24462  
probable 3',5'-cyclic-nucleotide phosphodiesterase (EC 3.1.4.17) R08D7.6 - Caenorhabditis  
N:Alternate names: hypothetical protein R08D7.6  
C:Species: Caenorhabditis elegans  
C>Date: 26-Aug-1999 #sequence\_revision 26-Aug-1999 #text\_change 09-Jul-2004  
C:Accession: S41041; S24462  
R:Ainscough, R.; Hawkins, T.  
submitted to the EMBL Data Library, May 1992  
A:Reference number: S41036  
A:Accession: S41041  
A:Molecule type: DNA  
A:Residues: 1-841 <AIN>  
A:Cross-references: UNIPROT:P30645; EMBL:Z12017  
R:Suleston, J.; Du, Z.; Thomas, K.; Wilson, R.; Hallier, L.; Staden, R.; Halloran, N.; G.  
awkins, T.; Ainscough, R.; Waterston, R.  
Nature 356, 37-41, 1992  
A:Title: The C. elegans genome sequencing project: a beginning.  
A:Reference number: S24457; MUID:92168156; PMID:1538779  
A:Contents: annotation  
C:Genetics:  
A:Introns: 31/3; 97/3; 179/2; 260/1; 296/3; 324/3; 622/2; 701/3; 775/3  
C:Superfamily: Caenorhabditis probable 3',5'-cyclic-nucleotide phosphodiesterase R08D7.3  
C:Keywords: phosphoric diester hydrolase  
P:403-627/Domain: 3',5'-cyclic-nucleotide phosphodiesterase homology <CNPD>  
Query Match 19.6%; Score 938; DB 1; Length 841;  
Best Local Similarity 33.1%; Pred. No. 3.4e-53;  
Matches 219; Conservative 120; Mismatches 226; Indels 96; Gaps 13;  
QY 250 NLQLSKCVIGDK-----VLEBEISPLTTGRLGQVVEDEKKSITQLKDLTSEDMDQLQSMGLG 304  
|||  
Db 72 NLQMLKRGTKDDWASLRVDIEPTSSGLL-ELLPD----- 108  
|||  
QY 305 CEVQAMLCVPVISRATQVVALACAFNKLGGDLFTDQDEHVIQHCFTVTSTVLTSLAPQ 364  
|||  
Db 109 -----VPIVKLSRPLVKM-----DQDDACSVAESNRDVTLSPLVPM 148  
|||  
QY 365 KEQKLKCEQALLQVAKNLFTHLDDVSVLQEIITEARNLSNAEICSVFLDQ----- 417  
|||  
Db 149 IFDQFLC-----LTNNL-----SALISCIATAEAKKTEADYAVFLHDEKNQMWL 194  
|||  
QY 418 --NE---LVAKVFDGQVVEDESYEIRIPADOGIAGHVATTTGQILNIPDAYAHLFVRGVD 472  
|||  
Db 195 FNNETMLTKGKFDWG-----YGIYGVKVASRTWMTNIRDVSRCPFFNEED 240  
|||  
QY 473 DSTGFRTRNLICFPKINENQVIGVAELVNKINGPWFSPKFDLATAFSIYCGISIAHSL 532  
|||  
Db 241 EQFSIKARNLIAFLIDSSCSLIGVIVLYNKENG--FSRDEKIKRFSYFVANSIAHAI 298  
|||  
QY 533 LYKKVNEAQYSHLANEMMY--HMKVSDDDEYTKLLHDGQIPVAIDSNFASFTYTPRSL 590  
|||  
Db 299 LAKQIEVTRIHVMVEEFKIQGEDAVIEEVDIMRLVNDPLRDWRYFSQNFADFPSPRSV 358  
|||





QY 474 STGPTNRILCPPIKNENQEVIGVAELVKNKINGPMFSEKFEDEDLATAPATSIYCGISIAHSLL 533  
DB DSGWITVKVNLSPPIVINKKEEIVGVATFYFNKDKGKFPDEQDEVLMSLTOFLGWSVLNTDT 434  
QY 534 YKVNVEAQRVSHLANEMMYHMK-----VSDEYTKLHLDGIQ 571  
DB 435 YDKMKLENRKDIAQDMVLYHVRCDREBIQLILPTRELRGKEPADCEDELGKILKEVLP 494  
QY 572 PVAALDSNFASTYTPRSLPEDDTSMALSLMDQNNFINNYKIDCPTLARFCLMVKKGYR 631  
DB 495 GPAKPD--IYEFHFSDELCTELELVKCGIQMYELGVVRKFOIPOEVLVRFVSXGKYR 552  
QY 632 DPPHYNHGASVSHFCVYLLKNELETNYLEMEIFALFISCMCHDLDRGCTNNSFOVAS 691  
DB 553 RITYHNWRHGFNAQTMFTLLMTGKLGKSYTDLFAPAMVTAAGLCHDIDHRGTNNLYQMK 612  
QY 692 KSVLAALYSSEGSVMERHFAQAIILNTHGNCIFDHFSRKDYQRMOLDMRDIIATDLA 751  
DB 613 QNPLAKLHGS--SILERHHLBFGKFLLSSETLNIYQNLRQHHEVHILMDIAIATDLA 670  
QY 752 HHLRIFKDLQMAE-----VGYDRTNKQHSLLCLLMTSCDLSQDTKGWKTTR 800  
DB 671 LYFKKRTWFOKIVDSKNVEDKSWVEYLSLETTREKEIVMAAMMTACDLSAITKPWEYQS 730  
QY 801 KIAELIYKEFFSQGLEK-AMGNRPMEWMDREK-AYIBELQISPMHEIAMPIYKLLQDLF 858  
DB 731 KVALLVAAEFWEQGLDERTVLDDQOPIPMMDRNKAAELPKLVGFIDFVCTFYKEFSRFH 790  
QY 859 PKAAELYERVASNRHWTQVSHKF--TIRGLPSNNSLDFLOBEYEVDPDLDGARAPINGCC 916  
DB 791 BEILPMFDRQLNRRKEWALADEYAKVAALEEDQKKTAKKVGTEICNGGPAPRSSTC 850  
QY 917 SL 918  
DB 851 RI 852  
RESULT 8  
I50186  
3',5'-cyclic-GMP phosphodiesterase (EC 3.1.4.35) - chicken  
C:Species: Gallus gallus (chicken)  
C:Date: 13-Sep-1996 #sequence\_revision 13-Sep-1996 #text\_change 09-Jul-2004  
C:Accession: I50186  
R:Sample-Rowland, S.L.; Green, D.A.  
Exp. Eye Res. 59, 365-372, 1994  
A:Title: Molecular characterization of the alpha'-subunit of cone photoreceptor cGMP phosphodiesterase  
A:Reference number: I50186; MUID:95121406; PMID:7821382  
A:Accession: I50186  
A:Status: preliminary; translated from GB/EMBL/DBJ  
A:Molecule type: mRNA  
A:Residues: 1-862 <SEN>  
A:Cross-references: UNIPROT:P52731; GB:L29233; NID:9495742; PIDN:AA42223.1; PID:9495743  
A:Superfamily: 3',5'-cyclic-GMP phosphodiesterase alpha chain; 3',5'-cyclic-nucleotide phosphodiesterase  
C:Keywords: cGMP binding; phosphoric diester hydrolase  
F:561-794/Domain: 3',5'-cyclic-nucleotide phosphodiesterase homology <NP>  
Query Match 16.7%; Score 799.5; DB 2; Length 862;  
Best Local Similarity 27.6%; Pred. No. 4e-44;  
Matches 219; Conservative 138; Mismatches 302; Indels 135; Gaps 24;  
QY 194 GDQKGVAYTNQDKILQCLGELYDL-----DASSLQI---KVLQYLOQETQASRCLL 244  
DB 42 GDVKEGVSFKMSR--LEECNIFLPTTEIQDEAGSMKEIVHKTQLRSLQLLRDCRSMF 99  
QY 245 LVS-----EDNLQLSCKVLGDKVLEBEISFPITTLTGRLGQVREDK 283  
DB 100 ICRSNGIPDEVATRLNLTPTSKFDNL-----VNPDK-----ETVPFLDIGIAGVATK 150  
QY 284 KSIQLKDLTSED--MQQLQSLMGCEVQAMLCVPVISRATQDVQVALACAFNKLGGDLFTDQ 341  
DB 151 KFFENIPDVKNHFDYLDKKTGYTTVNNMAIPITQ--GKEVLAVVMALNKLNASFEFSKE 208

QY 342 DERVIOHCFHYTSTVL-----TSTLAFQKEOKLCECOALLQVAKNLFTHLDDVSVLLQEI 397  
DB 209 DEEFVKYLVNIFSLVRNHTSYL--YNIESR---RSQMLLSANKVPFELTDIERQFHKA 264  
QY 398 ITEARNISNABICSVFLLDQNELVAKVPDGGV---EDES----- 435  
DB 265 LYTRMYLNCBRYSVGLLDMTK-EKEFYDEWPIRLGEAEPYKGPKTDPGREVNFYKIIDY 323  
QY 436 -----BIRI-----PAD-----QGIAGHVATTGOILNIPDAYA--HPLFYGVVDSTGPR 478  
DB 324 ILHGKEBIKVIPTPPADHWCLISGLPTYVAENGFCINMNAPEDEYFFQGPVDETMV 383  
QY 479 TRNLTCPPIKNENQEVIGVAELVKNKINGPMFSEKFEDEDLATAPATSIYCGISIAHSLLYKKNV 538  
DB 384 IKNVLSLPVINKKEIIVGVATFYFNKDKGKFPDEYDEQIIEITLTOFLGWSVLNTDTYDKN 443  
QY 539 BAQYRSHLANEMMYHMKVSDDEYTKLHLD-----GIQPVAAIDS----- 578  
DB 444 KLENRKDIAQEMLMYQTKATPTEVESILKYKEKLVNKSIEBCDEKDLIRILKEELPDPKD 503  
QY 579 -NFASFTYTPRSLPEDDTSMALSLMDQNNFINNYKIDCPTLARFCLMVKKGYRDPYPHN 637  
DB 504 LELYEPRFSDPPVTEHGLITCGIRLFEINVEFKVPAEVLTRWMTYTRVKGYRDITVHN 563  
QY 638 WMHAFSVSHFCVYLLKNELETNYLEMEIFALFISCMCHDLDRGCTNNSFOVASKSLAA 697  
DB 564 WRHGFNVQTMFTLLMTGRINKYTYDLEAFANVAAAFCHDIDHRGTNNLYQMKSNAPLAK 623  
QY 698 LYSSEGSVMERHFAQAIILNTHGNCIFDHFSRKDYQRMOLDMRDIIATDLAHLHRI 757  
DB 624 LHGS--SILERHHLBFGKFLLSSETLNIYQNLRQHHEVHILMDIAIATDLALYFKKR 681  
QY 758 KDLQMAE-----VGYDRTNKQHSLLCLLMTSCDLSQDTKGWKTTRKIA 803  
DB 682 TMFOKIVDAIEKMETEEEAIKYISIDPTKE---VIMAMMTGCDLSAITKPWEVQSVA 738  
QY 804 ELIYKEFFSQGLEK-AMGNRPMEWMDREK-AYIBELQISPMHEIAMPIYKLLQDLFPA 861  
DB 739 LMVANEWEQGLDERTVLDDQOPIPMMDRNKQDELPKLVGFIDFVCTFYKEFSRFHKEI 798  
QY 862 AELYERVASNRHWH 875  
DB 799 TPMFDGLQNNRVEW 812  
RESULT 9  
A47451  
3',5'-cyclic-GMP phosphodiesterase (EC 3.1.4.35) beta chain - dog  
C:Species: Canis lupus familiaris (dog)  
C:Date: 10-Sep-1999 #sequence\_revision 10-Sep-1999 #text\_change 09-Jul-2004  
C:Accession: A47451; S34290  
R:Suber, M.B.; Pittler, S.J.; Qin, N.; Wright, G.C.; Holcombe, V.; Lee, R.H.; Craft, C.M.  
Proc. Natl. Acad. Sci. U.S.A. 90, 3968-3972, 1993  
A:Title: Irish setter dogs affected with rod/cone dysplasia contain a nonsense mutation  
A:Reference number: A47451; MUID:93248211; PMID:8387203  
A:Accession: A47451  
A:Status: preliminary  
A:Molecule type: mRNA  
A:Residues: 1-856 <SUB>  
A:Cross-references: UNIPROT:P33726; GB:Z23014; NID:g312327  
A:Experimental source: Irish setter, retina  
A:Note: sequence inconsistent with the nucleotide translation  
R:Clements, P.J.  
submitted to the EMBL Data Library, June 1993  
A:Reference number: S34290  
A:Accession: S34290  
A:Status: preliminary  
A:Molecule type: mRNA  
A:Residues: 1-184; 'D', 186-856 <CLE>  
A:Cross-references: EMBL:Z23014; NID:g312327; PIDN:CAA80557.1; PID:g312328  
C:Superfamily: 3',5'-cyclic-GMP phosphodiesterase alpha chain; 3',5'-cyclic-nucleotide phosphodiesterase  
C:Keywords: cGMP binding; phosphoric diester hydrolase



F:556-789/Domain: 3',5'-cyclic-nucleotide phosphodiesterase homology <CNP>

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Query Match      16.7%; Score 799; DB 1; Length 856;
Best Local Similarity 26.5%; Pred. No. 4.2e-44;
Matches 223; Conservative 161; Mismatches 331; Indels 128; Gaps 24;

QY 189 PEEAGDQKGG-----VAYTNQDRKILQLQCLGELD-LDASSLQIKVLOYLQOETQ 237
DB 29 PEHVAGACDGGPTDCASRELQVBEESAAFLFELVQDMQESVNMERVVKILRLCTILR 88

QY 238 ASRCCILLVSDN--LQLSCKVIG---DKVLBE-----EISFPLTTGRLGQVVDKKS 285
DB 89 ADRCSLFWYRQNGVAELATRLFSVQPSGSALEDCLVPPDSEIVFPLDIDGVGHVATKKM 148

QY 286 IQLKDLTS--EDMQQLQSMGCEVQAMLCVPVISRATDQVVALACAFNKLGGDLFTDQDE 343
DB 149 VNVQDVTECPHFSPPADELGTGYNILATPIMN--GKEVAVIMALNKLGDGCPFTSEDE 206

QY 344 HVIQHCFHYTSTVLSTLAFQEKQKCEC---QALLQVAKNLFTHLDDVSVLLQEIITE 400
DB 207 DVF---LKYLNFGTLLKTYHLSYLHNCETRRGQVLLWSANKVFEELTDIERQPHKFTY 263

QY 401 ARNLNSNAETCSVFLDDQNELVAKVFDGGVV---EDESY----- 435
DB 264 VYAYLNCDRYSVGLLDMTK-EKEFFDVWVPLMGEAQPSGPRTPDGRREIVFVKVYDIILH 322

QY 436 ---EIRI-----PAD-----QGIAGHVATTGQILNPDAVAHPL--FYRGVDDSTGPR 481
DB 323 GKEDIKVIKIPSPADHWALASGLPTYVAESGFCINIMTADEMFTQEGPLDSDGVVKN 382

QY 482 ILCFPIKNEQVIGVAVELVKNKINGPWSKFPEDLATAFSICYGSIASHLSLYKKVNAEQ 541
DB 383 VLSMPEIVNKEBIVGATFYNRKDGKPFDEQDEVLMESLTQFLGWSVLNTDTYDKMKNLE 442

QY 542 YRSHLANEMMYHMKVSDDEYTKLHD---GIQPVAAIDSNFA----- 581
DB 443 NKQDIAQDMVLYHVRCDKDEIQELIPLTRERLKEPADCEDELGILLKEVLPGSKFDIY 502

QY 582 SFTYTPRSLPEDDTSMAILSMLQDMNFNNYKIDCPTLARFCLMVKKGYRDPYPYHNMHA 641
DB 503 EPHPSDLECTELELVKCGIQMYVELGVVRKFQIPQEVLRFLFSVSKGYRRITYHNRHG 562

QY 642 FSVSHFCYLLYKNLELTNYLEMEITPALFISCMCHDLHRGTNNNSFQVASKSVLAALYSS 701
DB 563 FNAVQTMFTLLTGLKSYTDLFAFAMVTAGLCHDHRGTNNLYQMSQNPFLAKLHGS 622

QY 702 EGSVMERHHFAQAIALLNTHGNCNIPDHFSRKYQYRMLDLWRDILATDLAHLRIFKDLQ 761
DB 623 --SILRHHLEFGKFLSSEETLNIYQNLNRQHEVHIHLMQIAITDIALYFKKRTWFO 680

QY 762 KMAE-----VGYDRTNKQHSLLLCILMTSCDLSDOTKGWKTTRKLAELIYKEF 810
DB 681 KIVDESKNYEDRSWVEYLSLETTKEIVWAMMTACDLSATKPEVQSKVALLVAEAF 740

QY 811 FSQGLEK-AMGNRPHEMMDREK-AVYPELQISFMEHIAMPYIKLLQDLFPKAAELYERV 868
DB 741 WEQGLERTVLQDQPIPMDRNKAELPKLQVGFDFVCTFYKFSRPHSEILPMFDR 800

QY 869 ASNREHWTKVSHKPTIRGLPSNNSLDPLDEEVEVD-----LDGARAPING-C 915
DB 801 QNKRKEWALADEYAK-----LKALEBEKQOQEDRTTAKKAGTEICNGGPAKSTFC 853

QY 916 CSL 918
DB 854 CIL 856
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RESULT 10

S30762

3',5'-cyclic-GMP phosphodiesterase (EC 3.1.4.35) beta chain - mouse

C:Species: Mus musculus (house mouse)

C:Date: 22-Nov-1993 #sequence revision 19-Oct-1995 #text\_change 09-Jul-2004

C:Accession: S30762; S13031; S13121

R:Baehr, W.

submitted to the EMBL Data Library, June 1991

A:Reference number: S30762

A:Accession: S30762

A:Status: preliminary

A:Molecule type: mRNA

A:Residues: 1-856 <BAE>

A:Cross-references: UNIPROT:P23440; EMBL:X60133; NID:G53595; PIDN:CAA42719.1; PID:G53596

R:Baehr, W.; Champagne, M.S.; Lee, A.K.; Pittier, S.J.

FEBS Lett. 278, 107-114, 1991

A:Title: Complete cDNA sequences of mouse rod photoreceptor cGMP phosphodiesterase alpha

cloning of the beta-subunit gene

A:Reference number: S13030; MUID:91130581; PMID:1847109

A:Accession: S13031

A:Status: preliminary

A:Molecule type: mRNA

A:Residues: 1-559, 'G', 561-856 <BA2>

A:Cross-references: EMBL:X60133

R:Bowes, C.; Li, T.; Danciger, M.; Baxter, L.C.; Applebury, M.L.; Farber, D.B.

Nature 347, 677-680, 1990

A:Title: Retinal degeneration in the rd mouse is caused by a defect in the beta subunit

A:Reference number: S13121; MUID:91015387; PMID:1977087

A:Accession: S13121

A:Molecule type: mRNA

A:Residues: 1-2, 'X', 4, 'G', 6-18, 'S', 20-48, 'DV', 51-157, 'T', 159-175, 'C', 177-231, 'R', 233-235

A:Cross-references: EMBL:X55968; NID:G53616; PIDN:CAA39439.1; PID:G53617

A:Note: The authors translated the codon AGA for residue 232 as Glu

C:Superfamily: 3',5'-cyclic-GMP phosphodiesterase alpha chain; 3',5'-cyclic-nucleotide

P:Keywords: cGMP binding; phosphoric diester hydrolase

F:556-789/Domain: 3',5'-cyclic-nucleotide phosphodiesterase homology <CNP>

Query Match 16.5%; Score 791; DB 2; Length 856;

Best Local Similarity 27.0%; Pred. No. 1.4e-43;

Matches 228; Conservative 159; Mismatches 325; Indels 134; Gaps 26;

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QY 189 PEEAGD-QKGVATNTQDRKILQL--CGELYDL-----DASSLQIKVLOYLQOETQ 237
DB 29 PENVAGACDGLADCGSLRELQVBEESAAFLFELVQDMQESVNMERVVKILRLCTILH 88

QY 238 ASRCCILLVSDN--LQLSCKVIG---DKVLBE-----EISFPLTTGRLGQVVDKKS 285
DB 89 ADRCSLFWYRQNGVAELATRLFSVQPSLLEDCLVPPDSEIVFPLDIDGVGHVATKKM 148

QY 286 IQLKDLT-----SEMQQLQSMGCEVQAMLCVPVISRATDQVVALACAFNKLGGDLFTD 340
DB 149 INVQDVABCSPPSSPADELTDV---TKNLTSTPMN--GKDVAVIMAVNKLGDGCPPTS 203

QY 341 QDEHVIQCHFYTSTVLSTLAFQEKQKCEC---QALLQVAKNLFTHLDDVSVLLQEI 397
DB 204 EDEDVFTTKYLNFAFLNLK---IYHLSYLHNCETRRGQVLLWSANKVFEELTDIERQFHKA 260

QY 398 ITEARNLSNAETCSVFLDDQNELVAKVFDGGVV---EDESY----- 435
DB 261 FYTTRAYLNCERYSVGLLDMTK-EKEFFDVWVPLMGEAQPSGPRTPDGRREIVFVKVYDI 319

QY 436 ---EIRI-----PAD-----QGIAGHVATTGQILNPDAVAHPL--FYRGVDDSTGPR 478
DB 320 ILHGKEDIKVIPTTPADHWALASGLPTYVAESGFCINIMNASADENFNFQEGPLDSDGVV 379

QY 479 TRNLCFPIKNEQVIGVAVELVKNKINGPWSKFPEDLATAFSICYGSIASHLSLYKKVN 538
DB 380 IKNVLSMPEIVNKEBIVGATFYNRKDGKPFDDQDEVLMESLTQFLGWSVLNTDTYDKMN 439

QY 539 EAQYRSHLANEMMYHMKVSDDEYTKLHD---GIQPVAAIDSNFA----- 581
DB 440 KLENKQDIAQDMVLYHVRCDKDEIQELIPLTRDRLKEPADCEDELGILLKEELPGPTKF 499

QY 582 ---SFTYTPRSLPEDDTSMAILSMLQDMNFNNYKIDCPTLARFCLMVKKGYRDPYPYHNM 638
DB 500 DIYRPHPSDLECTELELVKCGIQMYVELGVVRKFQIPQEVLRFLFSVSKAYRRITYHNM 559

QY 639 MHAFSVSHFCYLLYKNLELTNYLEMEITPALFISCMCHDLHRGTNNNSFQVASKSVLAAL 698
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Db 752 ERTVLOQPPMPMDENKEDLPKLVQGFIDFVCTFYVKEFRPHKEITPMLSLQGNRVE 811  
Qy 875 WTKVSHKFTIRGLPSNNSLDLDEE 899  
Db 812 WKSLADEYDAK-----MKVIEEE 829

RESULT 14  
S13032  
3',5'-cyclic-GMP phosphodiesterase (EC 3.1.4.35) beta' chain - mouse  
C:Species: Mus musculus (house mouse)  
C:Date: 21-Nov-1993 #sequence\_revision 10-Nov-1995 #text\_change 09-Jul-2004  
C:Accession: S13032; S30763  
R:Baehr, W.; Champagne, M.S.; Lee, A.K.; Pittler, S.J.  
FEBS Lett. 278, 107-114, 1991  
A:Title: Complete cDNA sequences of mouse rod photoreceptor cGMP phosphodiesterase alpha  
c'ing of the beta-subunit gene.  
A:Reference number: S13030; MUID:91130581; PMID:1847109  
A:Accession: S13032  
A:Molecule type: DNA  
A:Residues: 1-800 <BA>  
A:Cross-references: UNIPROT:Q62037; EMBL:X60133  
R:Baehr, W.  
submitted to the EMBL Data Library, June 1991  
A:Reference number: S30762  
A:Accession: S30763  
A:Molecule type: DNA  
A:Residues: 1-559,'R',561-800 <BA2>  
A:Cross-references: GB:X67952; EMBL:X60133; NID:q871432; PID:q871433  
C:Superfamily: 3',5'-cyclic-GMP phosphodiesterase alpha chain; 3',5'-cyclic-nucleotide P  
C:Keywords: alternative splicing; cGMP binding; phosphoric diester hydrolase  
F:556-790/Domain: 3',5'-cyclic-nucleotide phosphodiesterase homology <NP>

Query Match 15.8%; Score 756; DB 2; Length 800;  
Best Local Similarity 27.9%; Pred. No. 2.5e-41;  
Matches 216; Conservative 142; Mismatches 301; Indels 114; Gaps 23;

Qy 189 PEEAAGD-QKGGVATNQDRKILQI--CGEYIDL-----DASSLQKLVQLQGETQ 237  
Db 29 PENVAGACEDGLADCGSLRELCOVESAALFELVQDMQESVNMERVVFKILRLCTLH 88  
Qy 238 ASRCLLIVSDN--LQLSCVKIG--DKVLEE-----EISPLTTTGRGQVVEDKKS 285  
Db 89 ADRCSLFMYRGRNGIAELATRLFSVQPSLLEDCLVPPDSIVFPDLDIGVGHVAQYKGM 148  
Qy 286 IQLKDLT-----SEDMQOLQSMGLCEVQAMLCVPVISRATPDQVVALACAFNKLGGDLFTD 340  
Db 149 INVQDVASCPHFSSFADELTDVY---TKNILLSTPMN--GRQVAVIMAVNKLDPGCPFTS 203  
Qy 341 QDEHVIQCHFYTSTVLSTLAFOKEQKLKCEC---QALLQVAKNLFTHLDDVSVLLQEI 397  
Db 204 EDEDVFTKYLNFATLNK--IYHLSYLHNCETRGRGQVLLWSANKVFBEELTDIERQFHKA 260  
Qy 398 ITEARLNSAETCSFLLDQNELVAKVFDGGV--EDESY----- 435  
Db 261 FYTVRAYLNCBRYSGVLLDMTK-EKEFPDVPVLMGEAQPTSGRPTDPGRIVFYKVVDY 319  
Qy 436 -----EIRI-----PAD-----QGAGHVAATGQTINIPDAYAHL--FYRGVDSDTGFR 478  
Db 320 ILHGKEDIKVIPTTPADHWALASGLPTVVAESGFICINMNASADEMFNFQSGPLDDSGV 379  
Qy 479 TRNIIICFPKINENQEVIGVABLNVKINGPWFSGKFDDELATAFSYCGISIAHSLLYKKVN 538  
Db 380 IKNVLSMIPVKNKEIGVGVATFYNRKDGKFPDDQDELVMESLTOFLGWSVLNTDTYDKN 439  
Qy 539 EAQVRSHLANEMMYHMKVSDVEYTKLHD---GIQVVAALDSNFA----- 581  
Db 440 KLENKIDTAQDMVLTHVRCDKDETSQILPTDRDLGKEPADCEBELGKILKEELPGTKF 499  
Qy 582 ---SFTYTPRSLPEDDTSMAILSLQDMNFINNYKIDCPTTLARFCLMYKKGYRPPYHNW 638  
Db 500 DIYEFHPSDLCTELELVKCGIQMYELGVVRKFQIPQEVLRFLFSVKAYRRTIYHNW 559

Qy 639 MHAESVSHFCYLLYKNLELTNYLEDMEIFALFISCMCHDLDRGTNNNSFOVASKSVLAAL 698  
Db 560 GHGFNVATQMTFLTMTGKLKSYTTDLFAFAMVTAAGLCHDIDHRGTNNNDYQMKSQNPGLAKL 619  
Qy 699 YSSEGSVMERHFAQAIAIINTHGCNIFDHFSDKDYQRMMLDRDIIILATLAHLRIEKF 758  
Db 620 HGS--SILERHHLFEGKFLAABESLNIYQNLRQRHEVHILMDIAIATDLALYFKKRT 677  
Qy 759 DLQKMAE-----VGYDRTNKOHSLLLCLLMTSCDLSQDTGKWKTKRIAEILIY 807  
Db 678 MFQKIVDESKNYEDKKSWEYLSLETRKETVMAAMMTACDLSAITKPWEVQSKVALLVA 737  
Qy 808 KEFPSQGDLEK-AMGNRPMEKMDREK-AYIPELOISFMEHIAPIYKLLQDLF 858  
Db 738 ABFEWQGDLERTVLDQQPIPMMDRNKAABLPLQVGFIDFVCTFYVKEFRPHKEITPMLSLQGNRVE 790

RESULT 15  
S06418  
3',5'-cyclic-GMP phosphodiesterase (EC 3.1.4.35) alpha chain - bovine  
N:Alternate names: cGMP phosphodiesterase alpha chain  
C:Species: Bos primigenius taurus (cattle)  
C:Date: 30-Sep-1993 #sequence\_revision 30-Sep-1993 #text\_change 09-Jul-2004  
C:Accession: S06418; S27007; S00161; A34611; S08516  
R:Ovchinnikov, Y.A.; Gubanov, V.V.; Khramtsov, N.V.; Akhmedov, N.B.; Ishchenko, K.A.; Zha  
T.M.; Bystron, N.S.; Severtsova, I.V.; Lipkin, V.M.  
Dokl. Biochem. 296, 303-307, 1987  
A:Title: Cyclic GMP phosphodiesterase from bovine retina. Amino acid sequence of the alp  
A:Reference number: S06418  
A:Accession: S06418  
A:Molecule type: mRNA  
A:Residues: 1-859 <OV1>  
A:Cross-references: UNIPROT:P11541; EMBL:X12756; NID:g616; PIDN:CAA31243.1; PID:g617  
A:Accession: S27007  
A:Molecule type: protein  
A:Residues: 2-11;22-27;32-40;95-98;112-115;180-193;248-267;275-282;297-306;312-330;361-3  
645;654-663;663-667;703-712;734-736;751-760;766-771;787-798;811-819 <OV2>  
A:Note: this paper is a translation of the Russian paper published in Dokl. Akad. Nauk S  
R:Ovchinnikov, Y.A.; Gubanov, V.V.; Khramtsov, N.V.; Ishchenko, K.A.; Zagranichny, V.E.;  
FEBS Lett. 223, 169-173, 1987  
A:Title: Cyclic GMP phosphodiesterase from bovine retina. Amino acid sequence of the alp  
A:Reference number: S00161; MUID:98030033; PMID:2822478  
A:Accession: S00161  
A:Molecule type: mRNA  
A:Residues: 1-859 <OV2>  
A:Cross-references: EMBL:M27541; NID:g162826; PIDN:AAA30441.1; PID:g162828  
A:Note: part of this sequence was confirmed by protein sequencing  
A:Note: 381-Val was also found  
R:Pittler, S.J.; Baehr, W.; Waemuth, J.J.; McConnell, D.G.; Champagne, M.S.; vanTuinen,  
Genomics 6, 272-283, 1990  
A:Title: Molecular characterization of human and bovine rod photoreceptor cGMP phosphodi  
A:Reference number: A34611; MUID:90169986; PMID:2155175  
A:Accession: A34611  
A:Molecule type: mRNA  
A:Residues: 1-193,'V',195-423,'T',425-674,'F',676-859 <PIT>  
A:Cross-references: GB:M26043; NID:g162833; PIDN:AAA30443.1; PID:g162834  
C:Comment: This protein is involved in the transduction and amplification of the visual p  
C:Superfamily: 3',5'-cyclic-GMP phosphodiesterase alpha chain; 3',5'-cyclic-nucleotide P  
C:Keywords: acetylated amino end; cGMP; heterotrimer; phosphoric diester hydrolase; reti  
F:2-859/Product: 3',5'-cyclic-GMP phosphodiesterase alpha chain #status experimental <M  
F:558-791/Domain: 3',5'-cyclic-nucleotide phosphodiesterase homology <CNP>  
F:2/Modified site: acetylated amino end (Gly) (in mature form) #status experimental

Query Match 15.8%; Score 754.5; DB 1; Length 859;  
Best Local Similarity 25.8%; Pred. No. 3.5e-41;  
Matches 218; Conservative 148; Mismatches 335; Indels 145; Gaps 25;

Qy 189 PEEAAGDKGGVATNQDRKILQICGLHYDLDDASSLQKLVQLQYQQTQASRC----- 241  
Db 39 PREAAVD-----FSNYH-----ALNSVEEIEIFDLDRFDQNLQAEKCVFNVMKK 84  
Qy 242 -CLLLVSEDNLQLSC-----KVIGDKVLEE-----EISFPLTTTGRLGQ 278

Db 85 LCFL--QADRMSLPWRARGIAELATRLFNHVKDAVLEBCLVAPDSEIVFPLDMGVGH 143  
Qy 279 VVEDKKSIOQLDTSED---MQQLQSMGCEVQAMLCVPVISRATDQVVALACAFNKLGG 335  
Db 144 VALSKIVNVPN--TEEDEHCFDVTLTETQTKNILLASPIWN--GKDVVAIIMAVNKVDG 200  
Qy 336 DLFTDQDEHVIQHCPTHYSTVLTSTLAFQEQKLEKCEC---QALLQVAKNLFTHLDDVSV 392  
Db 201 PHTENDEEILLKYNLANIMK---VFHLSYLHNCETRRGQILLMSGSKVFEELTDIER 257  
Qy 393 LLOEIIITEARNLSNAEICSFLLDONELVAKVPD-----GGVVEDESYRIRI - 439  
Db 258 QFHKALYTVRAFLNCDRYSVGLLDMTK- QKEFFDVWVPLMGEAPPYAGPPTPDGREINFX 316  
Qy 440 -----PAD-----QGIAGHVATTGQILNIPDAYAHL--FYRGVDD 473  
Db 317 KVIDYILLHGKEDIKVPNPDPDHAWLVSGLPTVAQNGLICNIMNAPSEDFPAFQKEPLD 376  
Qy 474 STGFRTRNIIICPIKNEQVIGVAELVNKINGPWFSCFDEDLATAFSYCGISIAHSL 533  
Db 377 ESGWMIKNVLSMPIVKNKEEIVGATFYNRKDGKPFDEMDETLMESLAQFLGWSVLNPD 436  
Qy 534 YKVNQAQVESHLANEMMYHMKVSDDEYTKLLHD---GIQVAAIDSNFA----- 581  
Db 437 YELMKNLENKDIPODMVKYHVCDNREIQITILKTREYVKGKPEWCEEEELAEILOGELP 496  
Qy 582 -----SFTYTPRSIPEDDTSMAILSMQDMNFNNYKIDCPTLARFCLMVYKGYRDP 633  
Db 497 DADKYEINKPHFSDLPLETELVKCGIQMYVELKVVDKPHIPOEALVRPMYSLSKGYRRI 556  
Qy 634 PYNNMHAFSVSHFCVLLYKNLELTNYLEDMEIPALFISCMCHDLDRGTNNSFQVASKS 693  
Db 557 TYHNRHGFNVGQTFSLVTKRYFTDLEALAMVTAFCFCHIDHRTGNLYQMKSQN 616  
Qy 694 VLAALYSSEGSVMERHHFAQAIALLNTHGNCNIFDHFPSKDYQRMOLDIMRDIILLATL 753  
Db 617 PLAKJHGS--SILERHHLEFGKTLRDESINI FQNLNRQHEHAHMMMDIAITATDALY 674  
Qy 754 LRIFKDLQKMAE-----VGVDRTNKQHHSLLLCLLMTSCDLSDOTKGWKT 799  
Db 675 CKKRTMFQKIVDOSKTYETQEQWTOYMLDOTRKE---IVMAMMTACDLSAITKPWEVQ 731  
Qy 800 RKIAELIYKEFFSQDLEK-AMGNRPMEMMDREKA-YIPELQISFMHIAMPIYKLLQDL 857  
Db 732 SKVALLVAAEFWEQGLERTVLQONPIPMMDRNKADELPKLQVGFIDFVCTFVYKEFSRF 791  
Qy 858 FPKAAELYERVASNRHHTKVSHKP--TIRGLPSNNSLDFLDEEYVDPDLDGARAPING- 914  
Db 792 HEEITPMLDGIITNNRKWEKALADEYETKMKGLEEKQKQAAANQAAAGSQHGGKQPGGGP 851  
Qy 915 ---CC 916  
Db 852 ASKSCC 857

Search completed: June 26, 2005, 12:22:56  
Job time : 37.6393 secs

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GenCore version 5.1.6  
Copyright (c) 1993 - 2005 Compugen Ltd.

OM protein - protein search, using sw model

Run on: June 26, 2005, 12:06:56 ; Search time 131.465 Seconds  
(without alignments)  
3669.244 Million cell updates/sec

Title: US-10-697-894-43  
Perfect score: 4911  
Sequence: 1 MGACGHSILCRSQYPAAR.....VFDLGRAPINGCCSLDAB 942

Scoring table: BLOSUM62  
Gapop 10.0 , Gapext 0.5

Searched: 1612378 seqs, 512079187 residues

Total number of hits satisfying chosen parameters: 1612378

Minimum DB seq length: 0  
Maximum DB seq length: 2000000000  
Post-processing: Minimum Match 0%  
Maximum Match 100%  
Listing first 45 summaries

Database : UniProt\_03.\*  
1: uniprot\_sprot.\*  
2: uniprot\_trembl.\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	4728.5	96.3	941	1 CN2A_HUMAN	O00408 homo sapien
2	4711.5	95.9	941	2 Q81W54	Q81W54 homo sapien
3	4657	94.8	921	1 CN2A_BOVIN	P14099 bos taurus
4	4418	90.0	928	1 CN2A_RAT	Q01062 rattus norv
5	4366.5	88.9	916	1 CN2A_MOUSE	Q92284 mus musculu
6	3345	68.1	685	2 Q6ZMR1	Q6ZMR1 homo sapien
7	1659.5	33.8	819	2 Q96076	Q96076 ephydratia f
8	1236	25.2	491	2 Q7Q4A0	Q7Q4A0 anophelies g
9	992	20.2	1544	2 Q8MQW0	Q8MQW0 drosophila
10	986	20.1	934	2 Q9HCR9	Q9HCR9 homo sapien
11	986	20.1	988	2 Q9S76	Q9S76 homo sapien
12	986	20.1	1018	2 Q9STW8	Q9STW8 drosophila
13	986	20.1	1131	2 Q9VFI9	Q9VFI9 drosophila
14	983	20.0	1365	2 Q9VJ79	Q9VJ79 drosophila
15	974	19.8	935	2 Q8VID6	Q8VID6 rattus norv
16	950	19.3	1088	2 Q7QB99	Q7QB99 anophelies g
17	938	19.1	856	2 Q6ZC7	Q6ZC7 caenorhabdi
18	938	19.1	859	1 YN56_CABEL	P30645 caenorhabdi
19	923	18.8	883	2 Q6S9E8	Q6S9E8 rattus norv
20	920.5	18.7	684	2 Q9GZY7	Q9GZY7 homo sapien
21	916.5	18.7	852	2 Q6S9E9	Q6S9E9 rattus norv
22	915.5	18.6	779	2 Q6FXH1	Q6FXH1 homo sapien
23	915	18.6	789	2 Q9ULW9	Q9ULW9 homo sapien
24	914	18.6	794	2 Q9QYJ6	Q9QYJ6 rattus norv
25	913.5	18.6	779	1 CN10_HUMAN	Q9Y233 homo sapien
26	912.5	18.6	788	2 Q9QYJ5	Q9QYJ5 rattus norv
27	908	18.5	796	2 Q69C21	Q69C21 mus musculu
28	907	18.5	843	2 Q7ZM87	Q7ZM87 brachydanio
29	906.5	18.5	685	2 Q8VID7	Q8VID7 rattus norv
30	906.5	18.5	773	2 Q7TFG1	Q7TFG1 mus musculu
31	906.5	18.5	779	2 Q9WV11	Q9WV11 mus musculu

32	906.5	18.5	790	2	Q8CA95	Q8CA95 mus musculu
33	906.5	18.5	797	2	Q7TFG2	Q7TFG2 mus musculu
34	901	18.3	653	2	Q6S9E6	Q6S9E6 rattus norv
35	901	18.3	714	2	Q6S9E7	Q6S9E7 rattus norv
36	899	18.3	714	2	Q9HCP9	Q9HCP9 homo sapien
37	897	18.3	657	2	Q9NTV4	Q9NTV4 homo sapien
38	845.5	17.2	576	2	Q9HB46	Q9HB46 homo sapien
39	841.5	17.1	581	2	Q8VID8	Q8VID8 rattus norv
40	821.5	16.7	854	1	CN2A_HUMAN	P35913 homo sapien
41	805.5	16.4	865	1	CN5A_CANFA	Q77746 canis fami
42	804.5	16.4	862	1	CNRC_CHICK	P52731 gallus gall
43	804	16.4	875	1	CN5A_HUMAN	Q76074 homo sapien
44	801.5	16.3	853	1	CN2A_BOVIN	P23439 bos taurus
45	799	16.3	856	1	CN2A_CANFA	P33726 canis fami

ALIGNMENTS

RESULT 1

CN2A\_HUMAN

ID CN2A\_HUMAN STANDARD; PRT; 941 AA.

AC O00408;

DT 15-JUL-1998 (Rel. 36, Created)

DT 15-JUL-1998 (Rel. 36, Last sequence update)

DT 05-JUL-2004 (Rel. 44, Last annotation update)

DE CGMP-dependent 3',5'-cyclic phosphodiesterase (EC 3.1.4.17) (Cyclic

DE GMP stimulated phosphodiesterase) (CGS-PDE) (CGSPDE).

GN Name=PDE2A;

OS Homo sapiens (Human)

OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;

OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.

OX NCBI\_TaxID=9606;

RN [1]

RP SEQUENCE FROM N.A. (ISOFORM PDE2A3).

RC TISSUE=Fetal brain, and Hippocampus;

RX MEDLINE=97354299; PubMed=9210593; DOI=10.1016/S0378-1119(97)00046-2;

RA Rosman G.J., Martins T.J., Sonnenburg W.K., Beavo J.A., Ferguson K.,

RA Loughney K.;

RT "Isolation and characterization of human cDNAs encoding a CGMP-

RT stimulated 3',5'-cyclic nucleotide phosphodiesterase.";

RL Gene 131:89-95(1997).

CC -!- FUNCTION: Hydrolyzes both cyclic AMP (cAMP) and cyclic GMP (cGMP).

CC -!- CATALYTIC ACTIVITY: Nucleoside 3',5'-cyclic phosphate + H(2)O =

CC nucleoside 5'-phosphate.

CC -!- SUBUNIT: Homodimer (By similarity).

CC -!- SUBCELLULAR LOCATION: Membrane-bound (Potential).

CC -!- ALTERNATIVE PRODUCTS:

CC Event-Alternative splicing; Named isoforms=3;

CC Comment=Additional isoforms seem to exist. Experimental

CC confirmation may be lacking for some isoforms;

CC Name=PDE2A3;

CC IsoId=O00408-1; Sequence=Displayed;

CC Name=PDE2A1;

CC IsoId=O00408-2; Sequence=Not described;

CC Name=PDE2A2;

CC IsoId=O00408-3; Sequence=Not described;

CC -!- TISSUE SPECIFICITY: Expressed in brain and to a lesser extent in

CC heart, placenta, lung, skeletal muscle, kidney and pancreas.

CC -!- SIMILARITY: Belongs to the cyclic nucleotide phosphodiesterase

CC family.

CC -!- SIMILARITY: Contains 1 GAF domain.

CC This SWISS-PROT entry is copyright. It is produced through a collaboration

CC between the Swiss Institute of Bioinformatics and the EMBL outstation -

CC the European Bioinformatics Institute. There are no restrictions on its

CC use by non-profit institutions as long as its content is in no way

CC modified and this statement is not removed. Usage by and for commercial

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CC or send an email to [license@sib-sib.ch](mailto:license@sib-sib.ch)).

CC -----

DR EMBL; U67733; AAC51320.1; -;

DR Genew; HGNC:8777; PDE2A.

```
DR MIM; 602658; -.
DR GO; 0004118; F:cGMP-stimulated cyclic-nucleotide phosphodi. . .; TAS.
DR InterPro; IPR003018; GAF.
DR InterPro; IPR003607; Met_phos_hydro.
DR InterPro; IPR002073; PDease.
DR Pfam; PF01590; GAF; 2.
DR Pfam; PF00233; PDease I; 1.
DR PRINTS; PR00387; PDIESTERASE1.
DR SMART; SM00065; GAF; 2.
DR SMART; SM00471; HDC; 1.
DR PROSITE; PS00126; PDease I; 1.
KW Alternative splicing; cGMP; Hydrolase; Membrane.
FT DOMAIN 372 550
FT DOMAIN 633 891 Catalytic (By similarity).
FT DOMAIN 941 AA; 105716 MW; 97976098487FD64E CRC64;
SQ SEQUENCE 941 AA; 105716 MW; 97976098487FD64E CRC64;

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Best Local Similarity 96.0%; Pred. No. 2e-273;
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DB 1 MGQACGHSILCSQOYPAARPAERGGQVFLKPDPEPPPPQPCADSLQDALLSLGSDIV 60
QY 61 AGLOAVKEALSAVLPKVTETVYTYLLDGSRLVCEPPHPELPQEGKVRQVAVISKRLLGCN 120
DB 61 SGLQRAVKEALSAVLPVETVYTYLLDGSRLVCEPPHPELPQEGKVRQVAVISKRLLGCN 120
QY 121 GLGPSDLPGKPLARLVAFLAPDQVTLVPLVDKAGAAVAVILVHCQGLSDNEWSLQAV 180
DB 121 GLGPSDLPGKPLARLVAFLAPDQVTLVPLVDKAGAAVAVILVHCQGLSDNEWSLQAV 180
QY 181 EKHTLVALKRVAQLQORRESSVAPENTQNPPEAAGDQKGVAYTDDRKILQLCGELYDL 240
DB 181 EKHTLVALKRVAQLQORRESSVAPENTQNPPEAAGDQKGVAYTDDRKILQLCGELYDL 240
QY 241 DASSLQLKVLQVLOQETOASRCCLLVSEDNLQLSCKVIGDKVLEERTSPFLTGRLLQGV 300
DB 241 DASSLQLKVLQVLOQETOASRCCLLVSEDNLQLSCKVIGDKVLEERTSPFLTGRLLQGV 300
QY 301 VEDKKSILKDLTSEDMMQOLSGCEVQAMLCVPVISRATDQVVALACAFNKLGGDLFT 360
DB 300 VEDKKSILKDLTSEDVQOLQSLGCEVQAMLCVPVISRATDQVVALACAFNKLGGDLFT 359
QY 361 DQDEHVIOQHCHYTSVLTSTLAFQKEQKLCEQALLOVAKNLFTHLDDVSVLLQHIIT 420
DB 360 DEDEHVIOQHCHYTSVLTSTLAFQKEQKLCEQALLOVAKNLFTHLDDVSVLLQHIIT 419
QY 421 EARLNSNAEICSVFLLDQNEILVAKVFDGVVDEDSYEIRIPADQGIAGHVATTGQILNIP 480
DB 420 EARLNSNAEICSVFLLDQNEILVAKVFDGVVDEDSYEIRIPADQGIAGHVATTGQILNIP 479
QY 481 DAYAHLFYRGVDDSTGFRTRNILLCPPIKNEQVEVIGVAELVNKINGFWFSKDFEDLATA 540
DB 480 DAYAHLFYRGVDDSTGFRTRNILLCPPIKNEQVEVIGVAELVNKINGFWFSKDFEDLATA 539
QY 541 FSIYCGISIAHSLLYKKVNEAQYRSHLANEMMMTHMKVSDDEYTKLLHDGQIPVAAIDSN 600
DB 540 FSIYCGISIAHSLLYKKVNEAQYRSHLANEMMMTHMKVSDDEYTKLLHDGQIPVAAIDSN 599
QY 601 FASFTYTPRSPLPDDTSMALLSMQDMNFINNYKIDCPTLARFCFLMWKGYRDPYNNWM 660
DB 600 FASFTYTPRSPLPDDTSMALLSMQDMNFINNYKIDCPTLARFCFLMWKGYRDPYNNWM 659
QY 661 HAFVSHPFCYLLYKNLELTNYLEDMEIPALFISCMCHDLDRGTNNNSQVASKSVLAALY 720
DB 660 HAFVSHPFCYLLYKNLELTNYLEDIEIPALFISCMCHDLDRGTNNNSQVASKSVLAALY 719
QY 721 SSEGVSVMRHHFAQAIALNTHGNCIFDHFGRKDYQRMQLMRDIIILATDLAHLRIFKD 780
DB 720 SSEGVSVMRHHFAQAIALNTHGNCIFDHFGRKDYQRMQLMRDIIILATDLAHLRIFKD 779
QY 781 LQKMAEVGYDRTNKQHHSLLCLLMTSCDLSQDKGWKTKTKIAELIYKBFPSQGDLEKA 840

Db 780 LQKMAEVGYDRTNKQHHSLLCLLMTSCDLSQDKGWKTKTKIAELIYKBFPSQGDLEKA 839
QY 841 MGNRPMMMDREKAYIPELQISFMEHIAMPIYKLLQDLFPKAAELYERVASNRHWTQVS 900
DB 840 MGNRPMMMDREKAYIPELQISFMEHIAMPIYKLLQDLFPKAAELYERVASNRHWTQVS 899
QY 901 HKFTIRGLPSNNSLDFLDEEYVDPDLGAPINGCCSLDAE 942
DB 900 HKFTIRGLPSNNSLDFLDEEYVDPDLGTRAPINGCCSLDAE 941

RESULT 2
Q8IW54 PRELIMINARY; PRT; 941 AA.
ID Q8IW54
AC Q8IW54
DT 01-MAR-2003 (TrEMBLrel. 23, Created)
DT 01-MAR-2003 (TrEMBLrel. 23, Last sequence update)
DT 01-MAR-2004 (TrEMBLrel. 26, Last annotation update)
DE Phosphodiesterase 2A, cGMP-stimulated.
GN Name=PDE2A;
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX NCBI_TaxID=9606;
RN [1]
RP SEQUENCE FROM N.A.
RC TISSUE=Brain;
RX MEDLINE=22388257; PubMed=12477932; DOI=10.1073/pnas.242603899;
RA Strausberg R.L., Feingold E.A., Grouse L.H., Derge J.G.,
RA Klausner R.D., Collins F.S., Wagner L., Shenmen C.M., Schuler G.D.,
RA Altschul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,
RA Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J., Haieh F.,
RA Diatchenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L.,
RA Scapleton M., Soares M.B., Bonaldo M.F., Casavant T.L., Scheetz T.B.,
RA Brownstein M.J., Uedin T.B., Toshiyuki S., Carninci P., Prange C.,
RA Raha S.S., Loquellano N.A., Peters G.J., Abramson R.D., Mullahy S.J.,
RA Bosak S.A., McEwan P.J., McKernan K.J., Malek J.A., Gunaratne P.H.,
RA Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,
RA Villalón D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A.,
RA Whiting J., Helton E., Kettman M., Madan A., Rodrigues S., Sanchez A.,
RA Blakesley R.W., Touchman J.W., Green E.D., Dickson M.C.,
RA Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M., Butterfield Y.S.,
RA Krywinski M.I., Stalska U., Smaluk D.B., Schmerch A., Schein J.E.,
RA Jones S.J., Marra M.A.;
RT "Generation and initial analysis of more than 15,000 full-length human
and mouse cDNA sequences."
RL Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903(2002).
RN [2]
RP SEQUENCE FROM N.A.
RC TISSUE=Brain;
RA Strausberg R.;
RA Submitted (DEC-2002) to the EMBL/GenBank/DBJ databases.
DR EMBL; BC040974; AAH40974.1; -.
DR GO; GO:0004114; F:3'; 5'-cyclic-nucleotide phosphodiesterase a. . .; IEA.
DR GO; GO:0003824; F:catalytic activity; IEA.
DR GO; GO:0007165; F:signal transduction; IEA.
DR InterPro; IPR003018; GAF.
DR InterPro; IPR003607; Met_phos_hydro.
DR Pfam; PF01590; GAF; 2.
DR Pfam; PF00233; PDease I; 1.
DR PRINTS; PR00387; PDIESTERASE1.
DR SMART; SM00065; GAF; 2.
DR SMART; SM00471; HDC; 1.
DR PROSITE; PS00126; PDease I; 1.
SQ SEQUENCE 941 AA; 105648 MW; 93028FC28CB54D6B CRC64;

Query Match          95.9%; Score 4711.5; DB 2; Length 941;
Best Local Similarity 95.6%; Pred. No. 2.1e-272;
Matches 901; Conservative 19; Mismatches 21; Indels 1; Gaps 1;
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QY 1 MCQACGHSILCRSQQYPAARPAEPGRGQQVFLKPDPEPPPPPCADSLQDALLSLGSDIV 60
DB 1 MCQACGHSILCRSQQYPAARPAEPGRGQQVFLKPDPEPPPPPCADSLQDALLSLGSDIV 60
QY 61 AGLOQAVKEALSAVLPKVTVTYLLDGSRLVCEPPELHPOEGKVRKAVLSRRLGNC 120
DB 61 SGLQRAVKEALSAVLPKVTVTYLLDGSRLVCEPPELHPOEGKVRKAVLSRRLGNC 120
QY 121 GLGPSDLPGKPLARLVAIPADPTQVLVPLVDKEAGAAVAVLVHCQGLSDNEEWSLQAV 180
DB 121 GLGPSDLPGKPLARLVAIPADPTQVLVPLVDKEAGAAVAVLVHCQGLSDNEEWSLQAV 180
QY 181 EKHITVALKRVQALQORESSVAPEATONPPBEAGDKGQVAYTODRKILQICELYDL 240
DB 181 EKHITVALKRVQALQORESSVAPEATONPPBEAGDKGQVAYTODRKILQICELYDL 240
QY 241 DASSILQKVLQVLOQETOASRCLLVSDNLQSKVIGDKVLEEEISFPLTTCRLGQV 300
DB 241 DASSILQKVLQVLOQETOASRCLLVSDNLQSKVIGDKVLEEEISFPLTTCRLGQV 300
QY 301 VEDKKSILQKOLTSQMLGCEVQAMLCVPISEATQVVALACAFNKLGGDLFT 360
DB 301 VEDKKSILQKOLTSQMLGCEVQAMLCVPISEATQVVALACAFNKLGGDLFT 360
QY 361 DODEHVIQHCFTYTSVLTSLAFQEKQKCECQALLQVAKNLFTHLDDVSVLQSIIT 420
DB 361 DODEHVIQHCFTYTSVLTSLAFQEKQKCECQALLQVAKNLFTHLDDVSVLQSIIT 420
QY 421 EARNLSNAEICSVFLDDQNELVAKVFDGQVDESVETIRIPADQGIAGHVAATGQLNIP 480
DB 421 EARNLSNAEICSVFLDDQNELVAKVFDGQVDESVETIRIPADQGIAGHVAATGQLNIP 480
QY 481 DAYAHLFVRGVDSTGFRTRNLCFPIKQENQEVIGVAELVKNKINGPWFSDLDATA 540
DB 481 DAYAHLFVRGVDSTGFRTRNLCFPIKQENQEVIGVAELVKNKINGPWFSDLDATA 540
QY 541 PSYICGISTAHSLLYKKVNEAQRSHLANEMMYHMKVSDDDYTKLLHDGQIPVAAIDSN 600
DB 541 PSYICGISTAHSLLYKKVNEAQRSHLANEMMYHMKVSDDDYTKLLHDGQIPVAAIDSN 600
QY 601 FASFTYTPRSIPEDDTSNAILSMLODMFNINNYKIDCPTLAFCLMVKKGYRDPYHNWM 660
DB 601 FASFTYTPRSIPEDDTSNAILSMLODMFNINNYKIDCPTLAFCLMVKKGYRDPYHNWM 660
QY 661 HAFVSHPFCYLLYKNLELTNYLDEMEIFALFISCMCHDLDRGTNNNSFOVASKSVLAALY 720
DB 661 HAFVSHPFCYLLYKNLELTNYLDEMEIFALFISCMCHDLDRGTNNNSFOVASKSVLAALY 720
QY 721 SSEGSMVRRHHPAQAIALNTHGCGNIFDHSRKYORMLDLMDRIILATDLAHLRIFKD 780
DB 721 SSEGSMVRRHHPAQAIALNTHGCGNIFDHSRKYORMLDLMDRIILATDLAHLRIFKD 780
QY 781 LQKMAEVGYDRNKKOHSLLCLLMTSCDLSQDTGKWTTRKIAELIYKEPFSQGLSKA 840
DB 781 LQKMAEVGYDRNKKOHSLLCLLMTSCDLSQDTGKWTTRKIAELIYKEPFSQGLSKA 840
QY 841 MGNRMEMMDREKAVIPELOISFMHIAPIYKLLQDLFPKAAELYERVASNRHWTQVS 900
DB 841 MGNRMEMMDREKAVIPELOISFMHIAPIYKLLQDLFPKAAELYERVASNRHWTQVS 900
QY 901 HKFTIRGLPSNNSLDFLDEEYVPLDGDARAPINGCCSLDAE 942
DB 901 HKFTIRGLPSNNSLDFLDEEYVPLDGDARAPINGCCSLDAE 942
```

## RESULT 3

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ID CN2A BOVIN STANDARD; PRT; 921 AA.
AC P14099; 028064;
DT 01-JAN-1990 (Rel. 13, Created)
DT 01-DEC-1992 (Rel. 24, Last sequence update)
DT 05-JUL-2004 (Rel. 44, Last annotation update)
DE cGMP-dependent 3',5'-cyclic phosphodiesterase (EC 3.1.4.17) (Cyclic
```

```
DE GMP stimulated phosphodiesterase) (CGS-PDE) (cGSPDE).
GN Name=PDE2A;
OS Bos taurus (Bovine).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Cetartiodactyla; Ruminantia; Pecora; Bovidae;
OC Bovinae; Bos.
OX NCBI_TaxID=9913;
RN [1]
RP SEQUENCE FROM N.A. (ISOFORM PDE2A1).
RX MEDLINE=91373395; PubMed=1654333;
RA Sonnenburg W.K., Mullaney P.J., Beavo J.A.;
RT "Molecular cloning of a cyclic GMP-stimulated cyclic nucleotide
RT phosphodiesterase cDNA. Identification and distribution of isoyme
RT variants.";
RL J. Biol. Chem. 266:17655-17661(1991).
RN [2]
RP SEQUENCE FROM N.A. (ISOFORM PDE2A3).
RX MEDLINE=91104948; PubMed=2176866;
RA le Trong H., Beier N., Sonnenburg W.K., Stroop S.D., Walsh K.A.,
RA Beavo J.A., Charbonneau H.;
RT "Amino acid sequence of the cyclic GMP stimulated cyclic nucleotide
RT phosphodiesterase from bovine heart.";
RL Biochemistry 29:10280-10288(1990).
RN [4]
RP SEQUENCE OF 613-694 AND 808-868.
RX MEDLINE=87092242; PubMed=3025833;
RA Charbonneau H., Beier N., Walsh K.A., Beavo J.A.;
RT "Identification of a conserved domain among cyclic nucleotide
RT phosphodiesterases from diverse species.";
RL Proc. Natl. Acad. Sci. U.S.A. 83:9308-9312(1986).
CC -!- FUNCTION: Hydrolyzes both cyclic AMP (cAMP) and cyclic GMP (cGMP).
CC -!- CATALYTIC ACTIVITY: Nucleoside 3',5'-cyclic phosphate + H(2)O =
CC nucleoside 5'-phosphate.
CC -!- SUBUNIT: Homodimer.
CC -!- SUBCELLULAR LOCATION: Membrane-bound (Potential).
CC -!- ALTERNATIVE PRODUCTS:
CC Event-Alternative splicing; Named isoforms=3;
CC Comment=Additional isoforms seem to exist;
CC Name=PDE2A1;
CC IsoId=P14099-1; Sequence=Displayed;
CC Name=PDE2A2;
CC IsoId=P14099-3; Sequence=Not described;
CC Name=PDE2A3;
CC IsoId=P14099-2; Sequence=VSP 004555;
CC -!- SIMILARITY: Belongs to the cyclic nucleotide phosphodiesterase
CC family.
CC -!- SIMILARITY: Contains 1 GAF domain.
CC -----
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CC -----
DR EMBL; M73512; AAA74559.1; -.
DR EMBL; L49503; AAA87353.1; -.
DR F01; A40981; A40981.
DR InterPro; IPR003018; GAF.
DR InterPro; IPR003607; Met_phos_hydro.
DR InterPro; IPR002073; PDEase.
DR Pfam; PF01590; GAF; 2.
DR Pfam; PF02333; PDEase_1; 1.
DR PRINTS; PR00387; PD1ESTERASE1.
DR SMART; SM00065; GAF; 2.
```



```
DR InterPro; IPR003018; GAF.
DR InterPro; IPR003607; Met_phos_hydro.
DR InterPro; IPR002073; PDEase.
DR Pfam; PF01590; GAF; 2.
DR Pfam; PF00233; PDEase I; 1.
DR PRINTS; PR00387; PDIESTERASE1.
DR SMART; SM00065; GAF; 3.
DR SMART; SM00471; HDC; 1.
DR PROSITE; PS00126; PDEASE I; 1.
KW Alternative splicing; cGMP; Hydrolyase; Membrane.
FT DOMAIN 360 538
FT CATALYTIC (By similarity).
FT CATALYTIC W -> R (in Ref. 2).
FT CONFLICT 646 646
FT CONFLICT 758 758
SQ SEQUENCE 928 AA; 104663 MW; EF0B8C1E266EAB18 CRC64;

Query Match 90.0%; Score 4418; DB 1; Length 928;
Best Local Similarity 92.4%; Pred. No. 6.e-255;
Matches 846; Conservative 31; Mismatches 33; Indels 6; Gaps 2;

QY 25 RQQVFLKPPDEPPPPQPCADSLQDALSLGSLGVIDVAGLQQAVKALSAVLPKVETVYTY 84
DB 18 RQQVFLKPPDE--PPQPCCADSLQDALSLGSLGVIDIAGLRQAQKDALSAVLPKVETVY 75
QY 85 LLGDSRLVCEPPELPOEGKVRKAVISRKGLGNGLGPDLPGKPLARLVAPLADPTQ 144
DB 76 LVGDSRLVCEPPELPOEGKVRKAVISRKGLGNGLGPDLPGKPLARLVAPLADPTQ 135
QY 145 VLVPLVKEAGAAVAVLVHCGQLSDNEEWSLQAVEKHTLVALKRVALQORESSVAPE 204
DB 136 VLVPLVKEAGAAVAVLVHCGQLSDNEEWSLQAVEKHTLVALKRVALQORESSVAPE 191
QY 205 ATQNPPEAAGQKQGVAYTQDQRKILQCGELYDLDSLSLQKLVQLQOETQASRCCL 264
DB 192 AVQNTSADPSEQDQKDEKGYTAHDKILQCGELYDLDSLSLQKLVQLQOETQATHCCL 251
QY 265 LLVSDNQLQSKVIGDKVLEIEIFPTLTGRLQGVQVEDKKSILQKLTSDMQQLQSM 324
DB 252 LLVSDNQLQSKVIGDKVLEIEIFPTLTGRLQGVQVEDKKSILQKLTSDMQQLQSM 311
QY 325 GCEVQMLCVPIRSATQVVALACAFNKLGGDLTDDQDEHVOICFHYTSVLTSLAF 384
DB 312 GCEVQMLCVPIRSATQVVALACAFNKLGGDLTDDQDEHVOICFHYTSVLTSLAF 371
QY 385 QKEQKLKCEQALQVAKNLFTHLDDVSVLQEIITEARNLSNABICSVFLLDQNELVAK 444
DB 372 QKEQKLKCEQALQVAKNLFTHLDDVSVLQEIITEARNLSNABICSVFLLDQNELVAK 431
QY 445 VFDGVDVDESEYIRIPADQGIAGHVATTGQILNIPDAYAHLFVYRGVDDSTGFRNRL 504
DB 432 VFDGVDVDESEYIRIPADQGIAGHVATTGQILNIPDAYAHLFVYRGVDDSTGFRNRL 491
QY 505 CFPKKNQEVIGVAVELNKGKPFKPEDLATAFSIYCGISTAHSLLYKKVNEAOYR 564
DB 492 CFPKKNQEVIGVAVELNKGKPFKPEDLATAFSIYCGISTAHSLLYKKVNEAOYR 551
QY 565 SHLANEMMYHMKVSDDEYTKLLHDGIQVAAIDSNFASFTYTPRSLPEDDTSMALLSML 624
DB 552 SHLANEMMYHMKVSDDEYTKLLHDGIQVAAIDSNFASFTYTPRSLPEDDTSMALLSML 611
QY 625 QDMNFINNYKIDCPTLAFCLMVKGYRDPYPVHNMHAFSVSHFCYLLYKNLENTYLED 684
DB 612 QDMNFINNYKIDCPTLAFCLMVKGYRDPYPVHNMHAFSVSHFCYLLYKNLENTYLED 671
QY 685 MEIPALFTSCCHDLDRGTNNSFOVASKSVLAALYSSEGSMERHHFAQAIATLTHGC 744
DB 672 MEIPALFTSCCHDLDRGTNNSFOVASKSVLAALYSSEGSMERHHFAQAIATLTHGC 731
QY 745 NIFDHFSSKDYQVMDLDRDILATDLAHLRIKDLQKMAEVGYDRTNKHSHLLCLL 804
DB 732 NIFDHFSSKDYQVMDLDRDILATDLAHLRIKDLQKMAEVGYDRTNKHSHLLCLL 791
QY 805 MTSCLSDQTKGKWTTRKIAELIYKEFFSQGDEKAMGNRPMEMDMREKAYIPELQISFM 864
```

## RESULT 5

## CN2A\_MOUSE

## ID

## CN2A\_MOUSE

## STANDARD;

## PRT;

## 916 AA.

## Q92254; Q8K2UL;

## DT 28-PEB-2003 (Rel. 41, Created)

## DT 25-OCT-2004 (Rel. 45, Last sequence update)

## DT 25-JAN-2005 (Rel. 46, Last annotation update)

## DE cGMP-dependent 3',5'-cyclic phosphodiesterase (EC 3.1.4.17) (Cyclic

## DE GMP stimulated phosphodiesterase) (CGS-PDE) (CGSPDE).

## GN Name=Pde2a;

## OS Mus musculus (Mouse);

## OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;

## OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.

## NCBI\_TaxID=10090;

## RN [1]

## RP SEQUENCE FROM N.A.

## RC TISSUE=Breast tumor;

## RX MEDLINE=22389257; PubMed=12477932; DOI=10.1073/pnas.242603899;

## RA Strausberg R.L., Fellngold E.A., Grouse L.H., Derge J.G.,

## RA Klausner R.D., Collins F.S., Wagner L., Shenmen C.M., Schuler G.D.,

## RA Altschul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,

## RA Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J., Hsieh P.,

## RA Diatchenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L.,

## RA Stapleton M., Soares M.B., Bonaldo M.F., Casavant T.L., Schetz T.E.,

## RA Brownstein M.J., Usdin T.B., Toshiyuki S., Carninci P., Prange C.,

## RA Raha S.S., Loquellano N.A., Peters G.J., Abramson R.D., Mullahy S.J.,

## RA Boak S.A., McEwan P.J., McKernan K.J., Malek J.A., Gunaratne P.H.,

## RA Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,

## RA Villalon D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A.,

## RA Faney J., Helton E., Kettelman M., Madan A., Rodrigues S., Sanchez A.,

## RA Blakesley R.W., Touchman J.W., Green E.D., Dickson M.C.,

## RA Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M.,

## RA Butlerfield V.S.N., Krzywinski M.I., Skalska U., Smalios D.E.,

## RA Schnerch A., Schein J.E., Jones S.J.M., Marra M.A.;

## RT "Generation and initial analysis of more than 15,000 full-length human

## RT and mouse cDNA sequences.";

## RL Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903 (2002).

## RN [2]

## RP X-RAY CRYSTALLOGRAPHY (2.86 ANGSTROMS) OF 183-549 IN COMPLEX WITH GMP,

## RP AND DIMERIZATION.

## RX PubMed=12271124; DOI=10.1073/pnas.192374899;

## RA Martinez S.E., Wu A.Y., Glavas N.A., Tang X.-B., Turley S.,

## RA Hol W.G.J., Beavo J.A.;

## RT "The two GAF domains in phosphodiesterase 2A have distinct roles in

## RT dimerization and in cGMP binding.";

## RL Proc. Natl. Acad. Sci. U.S.A. 99:13260-13265 (2002).

## CC -I- FUNCTION: Hydrolyzes both cyclic AMP (cAMP) and cyclic GMP (cGMP)

## CC (By similarity).

## CC -I- CATALYTIC ACTIVITY: Nucleoside 3',5'-cyclic phosphate + H(2)O =

## CC nucleoside 5'-phosphate.

## CC -I- SUBUNIT: Homodimer.

## CC -I- SUBCELLULAR LOCATION: Membrane-bound (Potential).

## CC -I- SIMILARITY: LOCATION: The cyclic nucleotide phosphodiesterase

## CC family.

## CC -I- SIMILARITY: Contains 1 GAF domain.

## CC -----

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CC	-----	
DR	EMBL; BC006845; AAH06845.1; -;	
DR	EMBL; BC029810; AAH29810.1; -;	
DR	EMBL; BC057029; -; NOT_ANNOTATED_CDS.	
DR	PDB; 1MCO; X-ray; -;	
DR	MGD; MGI:2446107; Pde2a.	
DR	InterPro; IPR002073; PDEase.	
DR	Pfam; PFO0233; PDEase_I; 1.	
DR	PRINTS; PR00387; PDIESTERASE1.	
DR	PROSITE; PS00126; PDEASE_I; 1.	
KW	3D-structure; cGMP; Hydrolyase; Membrane.	
	GAF.	
FT	DOMAIN 348 526	
FT	DOMAIN 609 867	Catalytic (By similarity).
FT	SITE 421 422	GMP binding.
FT	BINDING 407 407	GMP.
SQ	SEQUENCE 916 AA; 103287 MW; 51C03B086633BF20 CRC64;	

Query Match 88.9%; Score 4366.5; DB 1; Length 916;  
Best Local Similarity 90.5%; Pred. NO. 7.6e-252;  
Matches 839; Conservative 36; Mismatches 39; Indels 13; Gaps 3;

Qy	14	QOYPAAPAPBPGQOVFLKDPDEPPPPQPCADSLQDALLSLGVSVIDVAGLQOAVKEALSA	73
Db	2	RRQPA--SQDPQAOK-----PEPFGSRDRRLLEDALLSGAVIDTAGLQAARDALSA	52
Qy	74	VLPKVETVTVYLLDGESRLVCEBPPHELPOBQKQVREAVISKRKLGCGNGLGSPDLPGKPLA	133
Db	53	VLPKVETVTVYLLDGESRLVCEBPPHELPOBQKQVREAVISOKRUSCNGLSGSPDLGLGPLA	112
Qy	134	RLVAPLAPDQVLVILPVLDEKAGAAVAVILVHCQQLSDNEBSWSQAQVEKHTLVALKRVOA	193
Db	113	RLVAPLAPDQVLVILPDLKETSVAAVILVHCQQLSDSEBSQSQQVVEKHALVALRRVOA	172
Qy	194	LQORESSVAPEATONPPEBAAGQKGVVYTDQDRKILQLCGELYDLDASLSQLKVLQYL	253
Db	173	LQORR----PEAVQNTSVDASEQDBKGYTDHDKILQLCGELFDLDATSLQLKVLQYL	228
Qy	254	QOETQASRCCLLIVSEONLQLSCKVIGDKVLEESI SPPLATITGRLOGVVEDKKSLQLKDLT	313
Db	229	QOETQATHCCLLLVSEONLQLSCKVIGDKVLGEBSVPLTNGRLOGVVEDKQCQLKDLT	288
Qy	314	SEDMMQQLSQMLGCSBVQAMLCPVVISRATDQVVALACAFNKLGGDLFTDQDEHVTHQCFHY	373
Db	289	SDDVQQLQNLMLGCELQAMLCPVVISRATDQVVALACAFNKLGGDFFTDEDEHVTHQCFHY	348
Qy	374	TSTVLTSTLAFQKQBOKLKCCEQALLQVAKNLFTHLDDVSVLLQBIITEARNLSNAEICSV	433
Db	349	TGTVLTSTLAFQKQBOKLKCCEQALLQVAKNLFTHLDDVSVLLQBIITEARNLSNAEICSV	408
Qy	434	FLLDQNELVAKVFGGVVDESEYIRIPADQGIAGHVATTQOILINIIPDAYAHPILFYRGVD	493
Db	409	FLLDQNELVAKVFGGVVDDSEYIRIPADQGIAGHVATTQOILINIIPDAYAHPILFYRGVD	468
Qy	494	DSTGFRTRNIIICPPIKKNENQBVIGVAELVNKINGPWFSPKDPEDLATAFSIYCGISIAHSL	553
Db	469	DSTGFRTRNIIICPPIKKNENQBVIGVAELVNKINGPWFSPKDPEDLATAFSIYCGISIAHSL	528
Qy	554	LYKKVNEAQYRSHLANEMMYTHMKVSDDGYTKLLHDDGIQPVAAIDSNFASFTYTPRSLPE	613
Db	529	LYKKVNEAQYRSHLANEMMYTHMKVSDDGYTKLLHDDGIQPVAAIDSNFANFTYTPRSLPE	588
Qy	614	DDTSMAILSMLQDNWFINNYKIDCPTLARFCIMVYKKGYPDPYNNWHAFFSVSHFCVILLY	673
Db	589	DDTSMAILSMLQDNWFINNYKIDCPTLARFCIMVYKKGYPDPYNNWHAFFSVSHFCVILLY	648
Qy	674	KNLELTWYLEDMEIFALFISCMWCHDLHRGNTNSFOVASKSVLAALYSSEGSVMERHHA	733
Db	649	KNLELSNYLEDIEIFALFISCMWCHDLHRGNTNSFOVASKSVLAALYSSEGSVMERHHA	708
Qy	734	QAIAILNTHGNCNIFDHFSRKDYQORMDLMRDIIILATDLAHLRILFXDLQKABRYGYDRTN	793

Db 102 ----- 101  
Qy 265 LLVSEDLQSKVIGDKVLEBESPLTTGRLGVQVEDKSGIQLKDLTSEDWQQLSML 324  
Db 102 ----- 101  
Qy 325 GCEVQMLCVPISRATDQVVALACAFNKLGGDLFTDQDEHVIOHCFHYTSTVLSTLAF 384  
Db 102 ----- 101  
Qy 385 QKEQKLKCEQALLQVAKNLFTHLDDVSLQBEIITEARNLSNAEICSFVLLDQNELVAK 444  
Db 128 QKEQKLKCEQALLQVAKNLFTHLDDVSLQBEIITEARNLSNAEICSFVLLDQNELVAK 187  
Qy 445 VPDGGVDESEYIIRIPADQGIAGHVATTGQILNIPDAYAHPLFYRGVDDSDGFRTRNL 504  
Db 188 VPDGGVDDSEYIIRIPADQGIAGHVATTGQILNIPDAYAHPLFYRGVDDSDGFRTRNL 247  
Qy 505 CPPIKNEQEVIGVAELVNKINGPWFSEKDEDLATAFSYCGISIAHSLLYKKVNEAQYR 564  
Db 248 CPPIKNEQEVIGVAELVNKINGPWFSEKDEDLATAFSYCGISIAHSLLYKKVNEAQYR 307  
Qy 565 SHLANEMMYHMKVSDDEYTKLLHDLGIQVAAIDSNFASFTYTPRSLPDDTSMALLSML 624  
Db 308 SHLANEMMYHMKVSDDEYTKLLHDLGIQVAAIDSNFASFTYTPRSLPDDTSMALLSML 367  
Qy 625 QDMNFNNYKIDCPTLARFCLMVKGYRDPYPYHNMHAFSVSHFCYLLYKNELTNYLED 684  
Db 368 QDMNFNNYKIDCPTLARFCLMVKGYRDPYPYHNMHAFSVSHFCYLLYKNELTNYLED 427  
Qy 685 MEIPALFISCMCHDLHRTGNNNSFQVASKSVLAALYSSEGSVWERHHFAQAIILNTHGC 744  
Db 428 IEIPALFISCMCHDLHRTGNNNSFQVASKSVLAALYSSEGSVWERHHFAQAIILNTHGC 487  
Qy 745 NIFDHPFRKDYORMLDLMDIILATDLAHLRIFKDLQKMAEVGYDRTNKHSHLLCLL 804  
Db 488 NIFDHPFRKDYORMLDLMDIILATDLAHLRIFKDLQKMAEVGYDRTNKHSHLLCLL 547  
Qy 805 MTSCLSDQTKGKTKRIKAEIYKEFFSQGLEKAMGNRPMEMDMREKAYIPELQISPM 864  
Db 548 MTSCLSDQTKGKTKRIKAEIYKEFFSQGLEKAMGNRPMEMDMREKAYIPELQISPM 607  
Qy 865 EHIAMPIYKLDLPFKAELYERVANSREHRTKSHKFTIRGLSPNSNLSLDFLDBEYV 924  
Db 608 EHIAMPIYKLDLPFKAELYERVANSREHRTKSHKFTIRGLSPNSNLSLDFLDBEYV 667  
Qy 925 DLDGARAPINGCCSLDAE 942  
Db 668 DLDGARAPINGCCSLDAE 685

RESULT 7  
096076

ID 096076 PRELIMINARY; PRT; 819 AA.  
AC 096076;  
DT 01-MAY-1999 (TremBLrel. 10, Created)  
DT 01-MAY-1999 (TremBLrel. 10, Last sequence update)  
DT 01-MAR-2004 (TremBLrel. 26, Last annotation update)  
DE EPPDE2  
OS Ephydactia fluviatilis.  
OC Eukaryota; Metazoa; Porifera; Demospongiae; Ceractinomorpha;  
OC Haplosclerida; Spongiillidae; Ephydactia.  
OX NCBI TaxId=31330;  
RN [1]  
RP SEQUENCE FROM N.A.  
RX MEDLINE=99015760; PubMed=9801141; DOI=10.1016/S0014-5793(98)01150-8;  
RA Koyanagi M., Suga H., Hoshiyama D., Ono K., Iwabe N., Kuma K.,  
RA Miyata T.;  
RT "Ancient gene duplication and domain shuffling in the animal cyclic  
RT nucleotide phosphodiesterase family.";  
RL FEBS Lett. 436:323-328(1998).  
RL EMBL; AB017022; BAA34308.1; -.  
DR GO; GO:0004114; F:3',5'-cyclic-nucleotide phosphodiesterase a. . .; IEA.

DR GO; GO:0003824; F:catalytic activity; IEA.  
DR GO; GO:0007165; P:signal transduction; IEA.  
DR InterPro; IPR003018; GAF.  
DR InterPro; IPR003607; Met\_phos\_hydro.  
DR InterPro; IPR02073; PDEase.  
DR Pfam; PF01590; GAF; 2.  
DR Pfam; PF00233; PDEase\_I; 1.  
DR PRINTS; PR00387; PDIESTERASE1.  
DR SMART; SM00065; GAF; 2.  
DR SMART; SM00471; HDC; 1.  
DR PROSITE; PS00126; PDEASE\_I; 1.  
SQ SEQUENCE 819 AA; 92145 MW; F4CALBESB23A9E0E CRC64;  
Query Match 33.8%; Score 1659.5; DB 2; Length 819;  
Best Local Similarity 40.3%; Pred. No. 2.2e-90;  
Matches 351; Conservative 160; Mismatches 265; Indels 95; Gaps 11;  
Qy 41 QPCADSL---QDALLSLGSDVIDVAGLQQAQKALSAVLPKVETVYTYLLDGSRLVC--- 94  
Db 13 RPSVALSGYEDAILGMGAAMSPTFTAAKGLCLRTFTSSMSAGVALLDNTENNELAYFE 72  
Qy 95 -EPPHELPEQEGKREAVISRKRKLCNGCLGSPDLPGKPLARLVAPLAPDTQVLVPLVDK 153  
Db 73 ENDKYTHLPKGVVWDVQR----- 93  
Qy 154 EAGAAVAILVHCGQLSDNEEWSLQAEKHTLVALKRVQALQOORESSVAPEATQNPBEA 213  
Db 94 -----TLEENYE-RLRLERTTLVAARVLAHLNSEH-----EKK 127  
Qy 214 AGDQKGVAYTDDQRKILQCGELYDLDASSLQLQVLQVLOQETQASRCLLVSEDLNQ 273  
Db 128 RID-----NMLRVCGELIDLDVVSLSIKLKHIMEVSNNAKCTLFYVEDVTQE 175  
Qy 274 LSCKVGIDKVLBEESFPLTTGRLGVQVEDKKSIOQLKOLTSQDMQ---QLQSLMGCEVQA 330  
Db 176 LVAYTYNGVPLDKERKPVSSSIYCECTTGLINISNV-PODMRNPNDITIKGYEPH 234  
Qy 331 MLCVPIR---ATDQVVALACAFNKLGGDLFTDQDEHVIOHCFHYTSTVLSTLAFQKE 387  
Db 235 LLCIPVKRGAQSGSVGLVVCNKNDRPTKHEDEGLYSLHFCSSMLNNTLVYQRE 294  
Qy 388 QKLKCEQALLQVAKNLFTHLDDVSLQBEIITEARNLSNAEICSFVLLD--QNELVAKV 445  
Db 295 LALKQNEVLLQVAKNLFSLDNLVSLRGNNAASSLTNAERCSLFLDKSRNLVATV 354  
Qy 446 PDGGVDESEYIIRIPADQGIAGHVATTGQILNIPDAYAHPLFYRGVDDSDGFRTRNLC 505  
Db 355 FNGDLKERTLTIKV--GGIAGYVAKGTIVNIIVDAQKHGQPPFAEVDKSTGFTKHLIC 412  
Qy 506 PPIKNEQEVIGVAELVNKINGPWFSEKDEDLATAFSYCGISIAHSLLYKKVNEAQYRS 565  
Db 413 PPIMDNNGVWGVAECLCNKNGKPTKYDEELARTFSAYCGISIVHSLKYETVMASSQGRS 472  
Qy 566 HLANEMMYHMKVSDDEYTKLLHDLGIQVAAIDSNFASFTYTPRSLPDDTSMALLSMLQ 625  
Db 473 SLATELMYLHKIRDELERATKTPLPVSSPHEMCKLTFSPDLKNSADSIANVMN 532  
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Db 533 EMDLINKQLPDLILARFVIMVKGYRDPYPYHNMHAFSVHFLYALYCCSKSLCLDDL 592  
Qy 686 EIFALFISCMCHDLHRTGNNNSFQVASKSVLAALYSSEGSVWERHHFAQAIILNTHGC 745  
Db 593 EVLALFVSLCHDIDHRTGNNNAFQVCSNSTLACYSSSEGSVWERHHLAQTCLILNSPGCN 652  
Qy 746 IPDHPFRKDYORMLDLMDIILATDLAHLRIFKDLQKMAEVGYDRTNKHSHLLCLL 805  
Db 653 IFENLSDYRTTIQLIQDNLDTDIASHLKLKHIKQWANDGYERSNEPHEHRLMCSLIM 712  
Qy 806 TSCDLSQTKGKTKRIKAEIYKEFFSQGLEKAMGNRPMEMDMREKAYIPELQISFME 865  
Db 713 TSCDLTASCKTWESKALSILYIYQFFSQGLEKALGVTPSEMMDRDRAPIFEQQLQFLD 772







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Db 831 AELVTSFEQGRERLEKLTPSAIFDRNRKDELPRLEWIDSICMPLYQALVKVNVK 890
Qy 882 AAEYERVASNRHWTGVSHKFTIRGLPSNNS 913
Db 891 LKPMDSVATNRSKWEELHQRLLASTASSSS 922

RESULT 11
Q96876 PRELIMINARY; PRT; 988 AA.
ID Q96876;
AC Q96876;
DT 01-DEC-2001 (TrEMBLrel. 19, Created)
DT 01-DEC-2001 (TrEMBLrel. 19, Last sequence update)
DE 01-MAR-2004 (TrEMBLrel. 26, Last annotation update)
DE Phosphodiesterase 11A3.
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX NCBI_TaxID=9606;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=20570133; PubMed=11121118;
RA Yuasa K., Kanch Y., Okumura K., Omori K.;
RT "Genomic organization of the human phosphodiesterase PDE11A gene;
RT Evolutionary relatedness with other PDEs containing GAF domains.";
RL Eur. J. Biochem. 268:168-178(2001).
DR EMBL; AB048423; BAB62713.1; -.
DR EMBL; AB048402; BAB62713.1; JOINED.
DR EMBL; AB048403; BAB62713.1; JOINED.
DR EMBL; AB048404; BAB62713.1; JOINED.
DR EMBL; AB048405; BAB62713.1; JOINED.
DR EMBL; AB048406; BAB62713.1; JOINED.
DR EMBL; AB048408; BAB62713.1; JOINED.
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DR EMBL; AB048415; BAB62713.1; JOINED.
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DR EMBL; AB048422; BAB62713.1; JOINED.
DR GO; GO:0004114; F:3',5'-cyclic-nucleotide phosphodiesterase a. . .; IEA.
DR GO; GO:0003824; F:catalytic activity; IEA.
DR GO; GO:0007165; P:signal transduction; IEA.
DR InterPro; IPR003018; GAF.
DR InterPro; IPR003607; Mec_phos_hydro.
DR Pfam; PF01590; GAF; 2.
DR Pfam; PF00233; PDEase I; 1.
DR PRINTS; PR00387; PDIESTERASE1.
DR SMART; SM00085; GAF; 2.
DR SMART; SM00471; HDC; 1.
DR PROSITE; PS00126; PDEASE_I; 1.
SQ SEQUENCE 988 AA; 111169 MW; 7F678869353DF7EB CRC64;

Query Match 20.1%; Score 986; DB 2; Length 988;
Best Local Similarity 30.7%; Pred. No. 4.4e-50;
Matches 249; Conservative 160; Mismatches 321; Indels 82; Gaps 19;

Qy 164 VHCQSLDSNEWSLQAVEKHTLVAKRVAQALQRESSVAP-----EATQNPPPE-- 211
Db 185 IHVNRTYD-EQVTSRAQPLSSV---RRALLRKASSLPPTAHLSALLSRLVNLQYP 240
Qy 212 BAAGDQKGGVAYTQDRKILQCGEL-YDLDASSLQLKVLQYLOQFTQASRCCLLLVSE 270
Db 241 PTAIDYKCHLKKHNRQPFLEVLVKDINSNLDLTSYKILIFVCLMVDADRCSLFLV--E 298
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RA Harris N.L., Harvey D., Heiman T.J., Hernandez J.R., Houck J.,  
RA Hostin D., Houston K.A., Howland T.J., Wei M.H., Ibegwam C.,  
RA Jalali M., Kalush F., Karpen G.H., Ke Z., Kennison J.A., Ketchum K.A.,  
RA Kimmel B.E., Kodira C.D., Kraft C., Kravitz S., Kulp D., Lai Z.,  
RA Laeko P., Lei Y., Levitsky A.A., Li J., Li Z., Liang Y., Lin X.,  
RA Liu X., Mattei B., McIntosh T.C., McLeod M.P., McPherson D.,  
RA Merkulov G., Milehina N.V., Mobarry C., Morris J., Moshrefi A.,  
RA Mount S.M., Moy M., Murphy B., Murphy L., Muzny D.M., Nelson D.L.,  
RA Nelson D.M., Nelson K.A., Nixon K., Nusskern D.R., Pacleb J.M.,  
RA Palazzolo M., Pittman G.S., Pan S., Pollard J., Puri V., Reese M.G.,  
RA Reinert K., Remington K., Saunders R.D., Scheeler F., Shen H.,  
RA Shue B.C., Siden-Kiamos I., Simpson M., Skupeki M.P., Smith T.,  
RA Spier E., Spradling A.C., Stapleton M., Strong R., Sun E.,  
RA Svirskas R., Tector C., Turner K., Venter E., Wang A.H., Wang X.,  
RA Wang Z.Y., Wasarman D.A., Weinstein G.M., Weissbach J.,  
RA Williams S.M., Woodagert, Worley K.C., Wu D., Yang S., Yao Q.A., Ye J.,  
RA Yeh R.F., Zaveri J.S., Zhan M., Zhang G., Zhao Q., Zheng L.,  
RA Zheng X.H., Zhong F.N., Zhong W., Zhou X., Zhu S., Zhu X., Smith H.O.,  
RA Gibbs R.A., Myers E.W., Rubin G.M., Venter J.C.;  
RT "The genome sequence of *Drosophila melanogaster*;"  
RL Science 287:2185-2195(2000).  
RN [2]  
RP SEQUENCE FROM N.A.  
RX MEDLINE=22426065; PubMed=12537568;  
RA Celnikier S.E., Wheeler D.A., Kronmiller B., Carlson J.W., Halpern A.,  
RA Patel S., Adams M., Champe M., Dugan S.P., Frise E., Hodgson A.,  
RA George R.A., Hoskins R.A., Laverty T., Muzny D.M., Nelson C.R.,  
RA Pacleb J.M., Park S., Pfeiffer B.D., Richards S., Sodergren E.J.,  
RA Svirskas R., Tabor P.E., Wan K., Stapleton M., Sutton G.G., Venter C.,  
RA Weinstein G., Scherer S.E., Myers E.W., Gibbs R.A., Rubin G.M.;  
RT "Finishing a whole-genome shotgun: Release 3 of the *Drosophila*  
RT melanogaster euchromatic genome sequence.";  
RL Genome Biol. 3:RESEARCH0079-RESEARCH0079(2002).  
RN [3]  
RP SEQUENCE FROM N.A.  
RX MEDLINE=22426070; PubMed=12537573;  
RA Kaminker J.S., Bergman C.M., Kronmiller B., Carlson J., Svirskas R.,  
RA Patel S., Frise E., Wheeler D.A., Lewis S.E., Rubin G.M.,  
RA Ashburner M., Celnikier S.E.;  
RT "The transposable elements of the *Drosophila melanogaster* euchromatin:  
RT a genomics perspective.";  
RL Genome Biol. 3:RESEARCH0084-RESEARCH0084(2002).  
RN [4]  
RP SEQUENCE FROM N.A.  
RX MEDLINE=22426069; PubMed=12537572;  
RA Misra S., Crosby M.A., Mungall C.J., Matthews B.B., Campbell K.S.,  
RA Hradecky P., Huang Y., Kaminker J.S., Millburn G.H., Prochnik S.E.,  
RA Smith C.D., Tupy J.L., Whitfield E.J., Bayraktaroglu L., Beriman B.P.,  
RA Bettencourt B.R., Celnikier S.E., de Grey A.D., Drysdale R.A.,  
RA Harris N.L., Richter J., Russo S., Schroeder A.J., Shu S.Q.,  
RA Stapleton M., Yamada C., Ashburner M., Gelbart W.M., Rubin G.M.,  
RA Lewis S.E.;  
RT "Annotation of the *Drosophila melanogaster* euchromatic genome: a  
RT systematic review.";  
RL Genome Biol. 3:RESEARCH0083-RESEARCH0083(2002).  
RN [5]  
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RG FlyBase;  
RL Submitted (SEP-2002) to the EMBL/GenBank/DBSJ databases.  
RN [6]  
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RG FlyBase;  
RL Submitted (MAR-2004) to the EMBL/GenBank/DBSJ databases.  
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DR FlyBase; FBgn0032686; Pdel1.  
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DR GO: GO:0003824; P:catalytic activity; IEA.  
DR GO: GO:0007165; P:signal transduction; IEA.  
DR InterPro; IPR003018; GAF.  
DR InterPro; IPR003607; Met\_phos\_hydro.  
DR InterPro; IPR002073; PDEase.  
DR Pfam; PF01590; GAF; 2.  
DR Pfam; PF00233; PDEase\_1; 1.

DR PRINTS; PRO0387; PDIBSTERASE1.  
DR SMART; SM00065; GAF; 2.  
DR PROSITE; PS00471; HGC; 1.  
DR PROSITE; PS00126; PDEase I; 1.  
SQ SEQUENCE 1365 AA; 151173 MW; B0562EPDF05012E56 CRC64;  
Query Match 20.0%; Score 983; DB 2; Length 1365;  
Best Local Similarity 31.2%; Pred. No. 1.1e-49;  
Matches 247; Conservative 150; Mismatches 307; Indels 88; Gaps 19;  
QY 225 DDDRILQICGEL-YDLASSLQLKVLQVLOQETASRCCLLV-----SENLQLSKV 278  
DB 290 DEKELIFELVKDICELEVRTLCHILQNVSTILLNADRGSLFLVQGRGNGPGLK-KCLV 348  
QY 279 -----IGDKVLEEEISFPLTTGRLGQVDEKKSQIKLQJLTDSEDM--QQLQSMGLG 325  
DB 349 SKLFDVCPRSTVEEMEQQDEVRAVGTGIAGHVAESGEPVNPIDAYQDERFNCEDSLTG 408  
QY 326 CEVQAMLCVPVSRATDQVVALACAFNKLGGDLPTDQDEHVHQHCFHYTSTVLTSLAFQ 385  
DB 409 YRTKALLCMPINKSSGD-VIGVAQVINKMNGECFSEIDEKVFSSYLQFCGIGLRNAQLYE 467  
QY 386 KEQKLKCECOALLOVAKNLFTHLDVSVLQELIITEARNLSNABICSVPLLDQNE--LVA 443  
DB 468 KSQLEIKRNVLLDLARIFEQSTIEHMFRLTHMQSLIOCORVOILLVHEADKGSFS 527  
QY 444 KVFD---GGVVEDES-----YEIRPADQGIAGHVAITGQILNIPDAYAHPLFYRGVDD 494  
DB 528 RVFDPENDLSEETSRTPSYESRFPINIGITGHVATTGETVNVNAYEDDRDFDASVDE 587  
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QY 555 YKKVNEAQYRSHLANEMMYMKVSDDEVTKL-----LHGD 590  
DB 648 YEKAIVAMAKQSVTLLEVLSYHASATMDEAHLRKQKQOQAVGLRQAPLSLPRKKLQRR 707  
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DB 768 YRNVYHNHRAFNVAQMMFALTTQWKIFGEIECLALIGCLCHDLDRGTNNNSFOI 827  
QY 711 ASKSVLAAALYSSEGSVMERHHPAQAIATLNTGCVIFDHFSEKDYQYRMLDLARDIILATD 770  
DB 828 KASSPLAQLYST--STMEHHHPDQCLMILNSPGNQLANLSSDDYCRVIRVLEDAILLSTD 885  
QY 771 LAHLRLIPKD---LQKMAEYGYDRTNKQHSLLCLLMTSCDLSQDTQKGMWTKTRKIAEL 826  
DB 886 LAVY---FKKGGPFLSVSQTYSYVAEPRALLRAMSMTVCDLSAITKPIWEIKRVADL 942  
QY 827 IYKEFFSGDLEKAMGN-RPMEMMDREKA-YIPELQISFMBHIAMPIYKLLQDLFPKAAE 884  
DB 943 VSSEFFEQDMKQELNITPIDINNRKEDBLPMQVNFIDSICLPIVEAFATLSDKLEP 1002  
QY 885 LYERVASNREHW-----TKVS-----HKFTIRGLPSNNSL-----DFLDESEYVP 924  
DB 1003 LVEGVRDNRGHWIDLADVTKTSQDQRPBEBEQOQNVISNGDCKAMSDDDVAASEAEVA 1062  
QY 925 -DLGGRAPING 935  
DB 1063 VDSPEKASVNG 1074  
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AC QVID6;  
DT 01-MAR-2002 (TRENBLrel. 20, Created)  
DT 01-MAR-2002 (TRENBLrel. 20, Last sequence update)



GenCore version 5.1.6  
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OM protein - protein search, using sw model

Run on: June 26, 2005, 12:09:51 ; Search time 32.3607 Seconds  
(without alignments)  
2800.810 Million cell updates/sec

Title: US-10-697-894-43  
Perfect score: 4911  
Sequence: 1 MGQACGSHILCSQQYPAAR.....VPDLGARAPINGCCSLDAE 942

Scoring table: BLOSUM62  
Gapop 10.0 , Gapext 0.5

Searched: 283416 seqs, 96216763 residues

Total number of hits satisfying chosen parameters: 283416

Minimum DB seq length: 0  
Maximum DB seq length: 2000000000  
Post-processing: Minimum Match 0%  
Maximum Match 100%  
Listing first 45 summaries

Database : PIR\_79:\*  
1: pir1:\*  
2: pir2:\*  
3: pir3:\*  
4: pir4:\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

## SUMMARIES

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1	4657	94.8	921	1 A40981	3',5'-cyclic-nucle
2	4418	90.0	928	1 JC2486	3',5'-cyclic-nucle
3	938	19.1	841	1 S24462	probable 3',5'-cyc
4	938	19.1	918	2 D88544	protein R08D7.6 (i
5	821.5	16.7	854	2 A42828	3',5'-cyclic-GMP p
6	804.5	16.4	862	2 I50186	3',5'-cyclic-GMP p
7	804	16.4	875	1 JW0106	3',5'-cyclic-GMP p
8	801.5	16.3	853	2 A36617	3',5'-cyclic-GMP p
9	801	16.3	856	1 A47451	3',5'-cyclic-GMP p
10	794	16.2	875	1 A48719	3',5'-cyclic-GMP p
11	791	16.1	856	2 S30762	3',5'-cyclic-GMP p
12	788	16.0	855	2 A34810	3',5'-cyclic-GMP p
13	758.5	15.4	858	2 JC4520	3',5'-cyclic-GMP p
14	756	15.4	800	2 S13032	3',5'-cyclic-GMP p
15	753.5	15.3	859	1 S06418	3',5'-cyclic-GMP p
16	739.5	15.1	859	2 S13030	3',5'-cyclic-GMP p
17	726	14.8	859	2 B34611	3',5'-cyclic-GMP p
18	696	14.2	393	2 T25590	hypothetical prote
19	401.5	8.2	859	2 AC2089	adenylate cyclase
20	390.5	8.0	664	2 T24459	hypothetical prote
21	383.5	7.8	712	2 S11626	3',5'-cyclic-nucle
22	382.5	7.8	673	2 I61358	3',5'-cyclic-nucle
23	381.5	7.8	549	2 T16769	hypothetical prote
24	380.5	7.7	584	2 B53109	3',5'-cyclic-nucle
25	380.5	7.7	672	2 I61259	3',5'-cyclic-nucle
26	380.5	7.7	886	2 A54442	3',5'-cyclic-nucle
27	379.5	7.7	536	2 I67945	3',5'-cyclic-nucle
28	379	7.7	562	2 I59143	cAMP phosphodiester
29	379	7.7	564	2 A40949	cyclic-AMP phospho

30	375	7.6	610	2 I67946	3',5'-cyclic-nucle
31	375	7.6	844	2 I53865	phosphodiesterase
32	374	7.6	564	2 JC1519	3',5'-cyclic-nucle
33	374	7.6	736	2 I61354	phosphodiesterase
34	363.5	7.4	777	2 S65543	3',5'-cyclic-nucle
35	350	7.1	519	2 T14783	hypothetical prote
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38	341.5	7.0	535	1 A44161	3',5'-cyclic-nucle
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43	329	6.7	267	2 B33904	cAMP phosphodiester
44	327	6.7	498	2 A47286	3',5'-cyclic-AMP p
45	325.5	6.6	323	2 S55348	3',5'-cyclic-nucle

## ALIGNMENTS

## RESULT 1

A40981  
3',5'-cyclic-nucleotide phosphodiesterase (EC 3.1.4.17), cGMP-stimulated - bovine  
N:Alternate names: cGMP-dependent phosphodiesterase  
C:Species: Bos primigenius taurus (cattle)  
C:Date: 26-Aug-1999 #sequence\_revision 26-Aug-1999 #text\_change 09-Jul-2004  
C:Accession: A40981; A36112; B26650; A60179; C26650  
R:Sonnenburg, W.K.; Mullaney, P.J.; Beavo, J.A.  
J. Biol. Chem. 266, 17655-17661, 1991  
A:Title: Molecular cloning of a cyclic GMP-stimulated cyclic nucleotide phosphodiesterase  
A:Reference number: A40981; MUID:91373395; PMID:1654333  
A:Accession: A40981  
A:Molecule type: mRNA  
A:Residues: 1-921 <SON>  
A:Cross-references: UNIPROT:P14099; GB:M73512; NID:9162829; PID:AAA74559.1; PID:g162830  
R:Lee Ironing, H.; Beier, N.; Sonnenburg, W.K.; Stroop, S.D.; Walsh, K.A.; Beavo, J.A.; Cha  
Biochemistry 29, 10280-10288, 1990  
A:Title: Amino acid sequence of the cyclic GMP stimulated cyclic nucleotide phosphodiester  
A:Reference number: A36112; MUID:91104948; PMID:2176866  
A:Accession: B36112  
A:Status: not compared with conceptual translation  
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A:Residues: 592-921 <LET>  
A:Accession: A36112  
A:Molecule type: protein  
A:Residues: 1-203, 'D', 205-477, 'Q', 479-921 <LET2>  
R:Charbonneau, H.; Beier, N.; Walsh, K.A.; Beavo, J.A.  
Proc. Natl. Acad. Sci. U.S.A. 83, 9308-9312, 1986  
A:Title: Identification of a conserved domain among cyclic nucleotide phosphodiesterases  
A:Reference number: A26650; MUID:87092242; PMID:3025833  
A:Accession: B26650  
A:Molecule type: protein  
A:Residues: 613-632, 'L', 634-794; 808-868 <CHA>  
A:Experimental source: heart  
R:Tanaka, T.; Hockman, S.; Moos Jr., M.; Taika, M.; Meacci, E.; Muraahima, S.; Manganieli  
Second Messengers Phosphoproteins 13, 87-98, 1991  
A:Title: Comparison of putative cGMP-binding regions in bovine brain and cardiac cGMP-st  
A:Reference number: A60179; MUID:92065414; PMID:1659635  
A:Accession: A60179  
A:Status: not compared with conceptual translation  
A:Molecule type: mRNA  
A:Residues: 311-803, 'DV', 806-921 <TAN>  
A:Note: part of this sequence was confirmed by protein sequencing  
C:Comment: This protein is not glycosylated.  
C:Superfamily: 3',5'-cyclic-nucleotide phosphodiesterase, cGMP-stimulated; 3',5'-cyclic-  
C:Keywords: acetylated amino end; alternative splicing; cAMP binding; cGMP binding; homo  
F:635-857/Domain: 3',5'-cyclic-nucleotide phosphodiesterase homology <CNPD>  
F:1/Modified site: acetylated amino end (Met) #status experimental

Query Match 94.8%; Score 4657; DB 1; Length 921;  
Best Local Similarity 98.9%; Pred. No. 3.4e-293;  
Matches 898; Conservative 3; Mismatches 7; Indels 0; Gaps 0;





QY 730 HFAQAIALNTHGCIPIHDFSRDYQRMGLDMDIILATDLAHLRIKFDLQMAEVGY 789  
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QY 790 DRTNQHSLLCLLMTSCDLSDOTKGWTKTKAELIYKEFFSGDLEKAMGNRPMEM 849  
Db 616 NPMSEFDRYLLMCLVNTASDLSQXKNFNKRAENIYLEFFAGDLELQGVKPLEMM 675  
QY 850 DREKAYIPELOISFMEHIAMPYIKLQDLFPKAAELYERVAENRHHWTKVSHKFTIRGLP 909  
Db 676 DRTNAYVPTQIDLEFKIGVDFVOLLASVPEGRITSEIDANHLWCWALDEE--VRNRP 733  
QY 910 S 910  
Db 734 S 734

RESULT 5  
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3',5'-cyclic-GMP phosphodiesterase (EC 3.1.4.35) beta chain - human  
C:Species: Homo sapiens (man)  
C:Date: 04-Mar-1993 #sequence revision 18-Nov-1994 #text\_change 09-Jul-2004  
C:Accession: A42828; S34590; S18715  
R:Collins, C.; Hutchinson, G.; Kowbel, D.; Riess, O.; Weber, B.; Hayden, M.R.  
Genomics 13, 698-704, 1992  
A:Title: The human beta-subunit of rod photoreceptor cGMP phosphodiesterase: complete re  
A:Reference number: A42828; MUID:92347868; PMID:1322354  
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A:Status: preliminary  
A:Molecule type: mRNA  
A:Residues: 1-854 <COL>  
A:Cross-references: UNIPROT:P35913; GB:S41458; NID:g252252; PIDN:AAB22690.1; PID:g252253  
A:Note: sequence extracted from NCBI backbone (NCBIN:109783, NCBI:P:109784)  
R:Khramtsov, N.V.; Feshchenko, E.A.; Suslova, V.A.; Shmukler, B.E.; Terpugov, B.E.; Raki  
FEBS Lett. 327, 275-278, 1993  
A:Title: The human rod photoreceptor cGMP phosphodiesterase beta-subunit. Structural stu  
A:Reference number: S34590; MUID:93351644; PMID:8394243  
A:Accession: S34590  
A:Status: preliminary  
A:Molecule type: mRNA  
A:Residues: 1-854 <KHR>  
A:Cross-references: EMBL:X66142; NID:g396492; PIDN:CAA46932.1; PID:g396493  
R:Weber, B.; Riess, O.; Hutchinson, G.; Collins, C.; Lin, B.; Kowbel, D.; Andrew, S.; S  
Nucleic Acids Res. 19, 6263-6268, 1991  
A:Title: Genomic organization and complete sequence of the human gene encoding the beta-  
A:Reference number: S18715; MUID:92066478; PMID:1720239  
A:Accession: S18715  
A:Status: preliminary  
A:Molecule type: DNA  
A:Residues: 1-314,'Q',316-319,'L',321-359,'R',361-697,'I',699-854 <WEB>  
A:Cross-references: EMBL:X62694  
C:Genetics:  
A:Gene: GDB:PDS6B; PDSE  
A:Cross-references: GDB:125915; OMIM:180072  
A:Map position: 4p16.3-4p16.3  
C:Superfamily: 3',5'-cyclic-GMP phosphodiesterase alpha chain; 3',5'-cyclic-nucleotide p  
C:Keywords: cGMP binding; phosphoric diester hydrolase  
F:556-789/Domain: 3',5'-cyclic-nucleotide phosphodiesterase homology <CNP>

Query Match 16.7%; Score 821.5; DB 2; Length 854;  
Best Local Similarity 27.5%; Pred. No. 5e-45;  
Matches 229; Conservative 158; Mismatches 326; Indels 119; Gaps 25;

QY 209 PPEAAGQKGGVAYTDQDRKIQLCGELYP-LDASSLQLKVLQVLOQETQASRCCLLLV 267  
Db 41 PPD---CDSLRDLQVEESTALLELVQDMQESINWVRFVLRRLCTLLQADRCSLFMY 97  
QY 268 SEDN--LQLSCKVTG---DKVLEE-----EISFPLTGRLGQVVEDKXSIQLKJDT-- 313  
Db 98 RQRNGVAELATRLFSVQDSVLEDCLPDPDSEIVFPDIDIGVVGHVQATKKMNVVEDVABC 157  
QY 314 ---SEDMQQLQSLGCEVQAMLCVPVISRATDQVVALACFNKLGDDLFTDQDEHVQHC 370

Db 158 PHFSFADELTDY---KTKMNLATPIMN--GKOVVAVIMAVNKLNGLFFSTSEDEDFVKY 212  
QY 371 PHYTSTVLTSLAFQKQKCEC---QALLQVAKNLFTHLLDDVSVLLQELIITEARNLSN 427  
Db 213 LNPATLYLK---IVHLSVYLNHCETRRGQVLWSANKVFEELTDIERQPHKAFYTVRAYLN 269  
QY 428 AETCSVELLDONELVAKVFGGVV---EDRSY-----EIR 459  
Db 270 CERYSGVLLDMTK-EKEFFDVMSVLMGESQPSGPRTPDGRHEIVFYKVIDYLHGKEIK 328  
QY 460 I----PAD----QGIAGHVATTGQILNIPDAYAHLPL--FYRGVDDSTGFRTRNLICPPI 508  
Db 329 VIPTPSADHWALASGLPSYVAESGFCINIMWASADEMPKFOEGALDGSGLIKVLSNPI 388  
QY 509 KNENQEVIGVAELVNKINGPMFSKFEDEDLATAFSICYGISTAHSLLYKKNVNEAQVRSHLA 568  
Db 389 VNKKEIVGVATFYNRKDGKPFDEQDEVLMESLTQFLGWSVMNTDTYDKMKNLENKRDIA 448  
QY 569 NEMMYMKVSDDEYTKLLHD----GIQPVNAIDSNFA-----SFTYTP 608  
Db 449 QDMVLYHVKCDRDEIQLIPTRARLKGEPADCDDEDELGEILKEBLPGCTTTFDIYEFHFS 508  
QY 609 RSLPEDDTSMAILSMLQDMNFNNYKIDCPTLARFCLMWKKGKGYRDPYPVNNMHAFSVGHF 668  
Db 509 LECTELDLVKCGIQNYTELGVKRFQIPQEVLVFLPSISKGYRRIYHNWRHGENVAQT 568  
QY 669 CYLLYKNLELTNYLEDMEIFALFISCMCHDLDRGTNNNSFQVASKSVLAALYSSEGSYME 728  
Db 569 MFTLLMTGKLSYYTDLEAFAMVTAGLCHDIDHRTNNLYQMKSONPLAKLHGS--SILE 626  
QY 729 RHHPAQAIATNTHGCIPIHDFSRDYQRMGLDMDIILATDLAHLRIKFDLQMAE-- 786  
Db 627 RHLEFQKFLSEETNIYQNLNRQHEVHILMDIAIATDLALYFKKRAMFOKIVDES 686  
QY 787 -----VGYDRTNKQHSLLLCLLMTSCDLSDOTKGWTKTKAELIYKEFFSQDGL 837  
Db 687 KNYQDKKSWEYLSLETRKEIVNMMWMTACDLSAITKFWPQSVQKVALVAEFWEQDGL 746  
QY 838 EK-AMGNRPMEMMDREK-AVYPELOISFMEHIAMPYIKLQDLFPKAAELYERVAENRHH 895  
Db 747 ERTVLDQOPIPMWDRNKAELPKLVGFIDFVCTFVYKEFSRFEHEILPMPDRLQNNRKE 806  
QY 896 WTKVSHKFTTRGLSPNNSLDFLDEYVDP-----LDGARAPING-CCSL 939  
Db 807 WKALADEYEAK----VKALEEKEEERVAACKVGTETCNGGPAPKPSSTCCIL 854

RESULT 6  
I50186  
3',5'-cyclic-GMP phosphodiesterase (EC 3.1.4.35) - chicken  
C:Species: Gallus gallus (chicken)  
C:Date: 13-Sep-1996 #sequence\_revision 13-Sep-1996 #text\_change 09-Jul-2004  
C:Accession: I50186  
R:Sample-Rowland, S.L.; Green, D.A.  
Exp. Eye Res. 59, 365-372, 1994  
A:Title: Molecular characterization of the alpha'-subunit of cone photoreceptor cGMP pho  
A:Reference number: I50186; MUID:95121406; PMID:7821382  
A:Accession: I50186  
A:Status: preliminary; translated from GB/EMBL/DBJ  
A:Molecule type: mRNA  
A:Residues: 1-862 <SEM>  
C:Superfamily: UNIPROT:P52731; GB:L29233; NID:g495742; PIDN:AAC42223.1; PID:g495743  
C:Keywords: cGMP binding; phosphoric diester hydrolase  
F:561-794/Domain: 3',5'-cyclic-nucleotide phosphodiesterase homology <CNP>

Query Match 16.4%; Score 804.5; DB 2; Length 862;  
Best Local Similarity 27.7%; Pred. No. 6.4e-44;  
Matches 220; Conservative 137; Mismatches 302; Indels 135; Gaps 24;

QY 215 GDQKGGVAYTDQDRKIQLCGELYDL-----DASSLQL---KVLQVLQETQASRCCLL 265











Db 60 LLEVLE-EAGSVELAAHRAALQRLAQLQADRCMSFLCRARNGTPEVASKLLDVTPTSKF 118  
QY 269 EDNLQLSCKVIGDKVLEEBISPLTTGRLGQGVVEDKKSQQLKDL--TSEDMQOQLMSLGC 326  
Db 119 EDNL-----VVPDR-----BAVFPDLVGIVGWAHTKTFNVPDVKNKSHFSPDMKQTCY 169  
QY 327 EQVAMLCVPVISRATDOVVALLACAFNKLGGDLFTDQDEHVIQHCFTYTSVLT---STLA 383  
Db 170 VTRNLATPIV--MGKEVLAVFMAVKNVDAASFQDEBFVSKYLSFVSIILKLHHTNYL 227  
QY 384 FQKEOKLKCECQALLQVAKNLFTHLDDVSQVLQQLQEIITEARNLSNAEICSFVLLDQNELVA 443  
Db 228 YNIESR---RSQILMWSANKVFEELTDERQHFALYVTRTYLNCERYSIGLDMWK-BK 283  
QY 444 KVFDDGW---BDESY-----EIRI-----PAD-----QGI 466  
Db 284 EFDWEPVKGVEPKPKTPDGREVIFYKIIDVILHGKEIKVPTPPMDHWTLLISGL 343  
QY 467 AGHVATTGQILNIPDAYA--HPLFYRGVDDSTGFRTRNLCPPIKNEQEVIGVAVLVNK 524  
Db 344 PTYVAENGFCNMLNAPADEYFTQKGPVDETGWIKNVLSPVINKKEDIVGVATFYNR 403  
QY 525 INGPWFSKPEDLATAFSYICGSIASHLSLYKKVNEAQVRSHLANEMMMHMKVSDDEYT 584  
Db 404 KDGKPFDEYDEHIAETLTQFLGWSLNTDTYKMKNKLENKRKDIAQEMLMNHTKATPDEIK 463  
QY 585 KLLH-----DGIQVAAIDSNFAS-----FTYTPRSIP--EDDTSMAILSM 623  
Db 464 SILKFKKLNIDVIEDCEBKQLVILKEDLPDPRADLYEPFRHLPITEHEHLIKGLRL 523  
QY 624 LQDMFPINNYKIDCPTLAFCLMVKGYRDPDPHYNNMHAFAFSVSHFCYLLYKNLELTNYLE 683  
Db 524 FPEINNVKFKVPEVVLTRWMTYTRKGYRAVTVYNNRHHGFNVGQWTFILLMTGLRKKYTT 583  
QY 684 DMEIFALFISCMCHDLDRGTNNNSFOVASKSVLAALYSSEGVSVERHHPAQAIATLHTG 743  
Db 584 DLFAFAMLAAPACHDIDHRGTNNLYQMKSTSPARLHGS--SILSRHLLYSKTLLODES 641  
QY 744 CNIPDHFSRKQYQRMLDLMDRIILATDLAHLIRIFKDLQKMAE-----VG 789  
Db 642 LNIFQNLNKRQVETVHLFEVAILIATDLALYFKKRTMQKIVDACEKMETEBEAIKYITI 701  
QY 790 DRNTKQHSLLLCLLMTSCDLSQDKGWKTTRKIAELIYKEFPFSGDLEK-AMGNRPMEM 848  
Db 702 DPTKKE---IIMAMMTACDLSAITKPWEVQSVQVALLVANEFWEQGLERTVLQQQPIPM 758  
QY 849 MDR-EKAYIPELQISFMEHIAMPIYKLLQDLFPKAAELYERVASNREHWTKVSHKF 903  
Db 759 MDRNKKDELPLKQVGFIDPVCTFYVYKEFSRFHKEITPMLNGLQNNRNVEMKSLADEY 814

RESULT 13  
JC4520  
3',5'-cyclic-GMP phosphodiesterase (EC 3.1.4.35) alpha' chain - human  
C:Species: Homo sapiens (nan)  
C>Date: 08-Feb-1996 #sequence\_revision 11-Apr-1997 #text\_change 09-Jul-2004  
C:Accession: S63688; JC4520  
R:Peschenko, E.A.; Andreeva, S.G.; Suslova, V.A.; Smirnova, E.V.; Zagranichny, V.E.; Li  
FEBS Lett. 381, 149-152, 1996  
A>Title: Human cone-specific cGMP phosphodiesterase alpha' subunit: complete cDNA sequen  
A:Reference number: S63688; MUID:96193933; PMID:8641425  
A:Accession: S63688  
A:Molecule type: mRNA  
A:Residues: 1-858 <FES>  
A:Cross-references: UNIPROT:P51160; EMBL:X94354; NID:g1616594; PIDN:CAA64079.1; PID:g114  
A>Note: Intron positions were determined by partial sequencing of genomic DNA  
R:Vicizian, A.S.; Piriev, N.I.; Farber, D.B.  
Gene 166, 205-211, 1995  
A>Title: Isolation and characterization of a cDNA encoding the alpha' subunit of human c  
A:Reference number: JC4520; MUID:96125191; PMID:8543163  
A:Accession: JC4520  
A:Molecule type: mRNA

A:Residues: 1-115, 'V', 117-269, 'S', 271-372, 'P', 374-463, 'L', 465-564, 'Q', 566-858 <VIC>  
A:Cross-references: GB:U31973; NID:g940230; PIDN:AAA96392.1; PID:g940231  
A>Note: this sequence lacks a residue Tyr after the 231-Met, and has an additional resi  
C:Genetics:  
A:Gene: alpha'-pde  
A:Introns: 160/3; 211/3; 241/3; 288/3; 313/3; 335/2; 357/3; 373/3; 423/3; 471/3; 494/3;  
C:Superfamily: 3',5'-cyclic-GMP phosphodiesterase alpha chain; 3',5'-cyclic-nucleotide  
C:Keywords: cGMP binding; lipoprotein; phosphoric diester hydrolase; photoreceptor; pre  
F:560-770/Domain: catalytic #status predicted <CAT>  
F:561-794/Domain: 3',5'-cyclic-nucleotide phosphodiesterase homology <CNPD>  
F:855/Binding site: geranyl-geranyl (Cys) (covalent) #status predicted

Query Match 15.4%; Score 758.5; DB 2; Length 858;  
Best Local Similarity 25.8%; Pred. No. 66-41;  
Matches 208; Conservative 151; Mismatches 299; Indels 147; Gaps 22;

QY 236 ELYDLDDASSLQIKVLYLQOE-----TQASRCLLIVS----- 268  
Db 52 ELTQVEESALCLLELLWTVQEEGTPQGVHRAQLRALHLLQADRCSMFLCRSNGIPEVA 111  
QY 269 -----EDNLQLSCKVIGDKVLEEBISPLTTGRLGQGVVEDKKSQQLKDL--TS 314  
Db 112 SRLLDVTPTSKPEDNL-----VGP---DKEVVPDLIDIGVGAHAHTKKTNNVPDVKNKNS 162  
QY 315 EDMQQLMSLGCVEQVAMLCVPVISRATDOVVALLACAFNKLGGDLFTDQDEHVIQHCFTY 374  
Db 163 HPSDFMDKQGTGYVTKNLLATPIV--VGKEVLAVFMAVKNVDAASFQDEBFVSKYLYN 220  
QY 375 STVLTL---STLAFQKEQKLKCECQALLQVAKNLFTHLDDVSQVLQQLQEIITEARNLSNAE 431  
Db 221 SIILLHTSYMYNIESR---RSQILMWSANKVFEELTDERQHFALYVTRTYLNCERY 277  
QY 432 SVFLLDQNELVAKVPDGGV---EDES-----EIRI----- 460  
Db 278 SIGLLDMTK-EKEFYDEWPIKLGVEPKPKTPDGREVNFYKIIDVILHGKEIKVPT 336  
QY 461 -PAD-----QGIAGHVATTGQILNIPDAYA--HPLFYRGVDDSTGFRTRNLCPPIKNE 512  
Db 337 PPADHWTLLISGLPTVVAENGFCNMLNAPADEYFTQKGPVDETGWIKNVLSPVINKK 396  
QY 513 QEVIGVAVLNKINGPWFSPKPEDLATAFSYICGSIASHLSLYKKVNEAQVRSHLANEM 572  
Db 337 EDIVGVATFYNRKQKPFDEHDEYITETLTQFLGWSLNTDTYKMKNKLENKRKDIAQEM 456  
QY 573 MYHMKVSDDEYTKLLH-----DGIQVAAI-----DSNFASFTYTPRSL 611  
Db 457 MNQTKATPEEIKSILKFOEKLNVVDVDDCEBKQLVAILKEDLPDPRSAELYEFPFSDPL 516  
QY 612 PEDDTSMAILSMQDMFINNYKIDCPTLAFCLMVKGYRDPDPHYNNMHAFAFSVSHFCYL 671  
Db 517 TEHGLIKGIRLFPFEINNVKFKVPEVVLTRWMTYTRKGYRAVTVYNNRHHGFNVGQWTF 576  
QY 672 LYKNLELTNYLEDMEI PALFISCMCHDLDRGTNNNSFOVASKSVLAALYSSEGVSVERH 731  
Db 577 LMTGRKKYTYDLEAFAMLAAPACHDIDHRGTNNLYQMKSTSPARLHGS--SILSRH 634  
QY 732 FAQAIAIANTHGCNIFDHFSRKQYQRMLDLMDRIILATDLAHLIRIFKDLQKMAE----- 786  
Db 635 LEYSKTLQDSSLNIFQNLNKRQVETVHLFEVAILIATDLALYFKKRTMQKIVDACEQM 694  
QY 787 -----VGYDRNTKQHSLLLCLLMTSCDLSQDKGWKTTRKIAELIYKEFPFSGDL 837  
Db 695 QTEBEAIKYVTVDP TKKE---IIMAMMTACDLSAITKPWEVQSVQVALLVANEFWEQGL 751  
QY 838 EK-AMGNRPMEMMDREKA-VIPELQISFMEHIAMPIYKLLQDLFPKAAELYERVASNREH 895  
Db 752 ERTVLQQQPIPMMDRNKRDELPLKQVGFIDPVCTFYVYKEFSRFHKEITPMLSGLQNNRVE 811  
QY 896 WTKVSHKFTIRGLPSNNSLDPLDEE 920  
Db 812 WKSLADEYDAK-----MKVIEE 829

```
RESULT 14
S13032
3',5'-cyclic-GMP phosphodiesterase (EC 3.1.4.35) beta' chain - mouse
C:Species: Mus musculus (house mouse)
C:Date: 21-Nov-1993 #sequence_revision 10-Nov-1995 #text_change 09-Jul-2004
C:Accession: S13032; S30763
R:Baehr, W.; Champagne, M.S.; Lee, A.K.; Pittler, S.J.
FEBS Lett. 278, 107-114, 1991
A:Title: Complete cDNA sequences of mouse rod photoreceptor cGMP phosphodiesterase alpha
      cing of the beta-subunit gene.
A:Reference number: S13030; MUID:91130581; PMID:1847109
A:Accession: S13032
A:Molecule type: DNA
A:Residues: 1-800 <BAE>
A:Cross-references: UNIPROT:Q62037; EMBL:X60133
R:Baehr, W.
submitted to the EMBL Data Library, June 1991
A:Reference number: S30762
A:Accession: S30763
A:Molecule type: DNA
A:Residues: 1-559,'R',561-800 <BA2>
A:Cross-references: GB:X87952; EMBL:X60133; NID:g871432; PIDN:CAA61202.1; PID:g871433
C:Superfamily: 3',5'-cyclic-GMP phosphodiesterase alpha chain; 3',5'-cyclic-nucleotide
C:Keywords: alternative splicing; cGMP binding; phosphoric diester hydrolase
F:556-790/Domain: 3',5'-cyclic-nucleotide phosphodiesterase homology <CNP>

Query Match      15.4%; Score 756; DB 2; Length 800;
Best Local Similarity 27.4%; Pred. No. 7.8e-41;
Matches 212; Conservative 145; Mismatches 302; Indels 114; Gaps 22;

Qy 210 PEEAGDQKGG-----VAYTDQDKILQGLGYD-LDASSLQKLVQYLOQBTQ 258
Db 29 PENVAGACEDWLDCGSLRELQVESAALFELVDQMSVNNRVERVFKLRLRLCTILH 88

Qy 259 ASRCLLVSDN--LQISCKVIG---DKVLEE-----BISPLTTGRLGQVVEDKKS 306
Db 89 ADRCSLFVYRQNGIAELATRLFSVQPDLSLLEDCLVPPDSEIVPPLDIGVGHVAQTCKM 148

Qy 307 IQLKDLT-----SEMQQLQSMGLGEVQAMLCVPVISRATQOVVALACAFNKLGGDLFTD 361
Db 149 INVQDVARECPHFSPADLTDYV---TKNILLSTPMN--GRDVAVIMAVNKLDPGPCPTS 203

Qy 362 QDEHVIQCHFYVTSVLTSTLFAQEQKLCCEC---QALLQVAKNLFTHLDDVSVLLQEI 418
Db 204 EDEDVFTKYNFATNLK---IYHLSYLHNCTETRGQVLLMSANKVFELTDIERQFKA 260

Qy 419 ITEARLNSABICSVFLDDQBNELVAKVPDGGV---EDES-----456
Db 261 FVTVRAYLNCERSYVGLLDMTK-EKEFPDVPVLMGEAQPYSGPRTPDGRBEIVFKYVDY 319

Qy 457 -----ETRI-----PAD-----QGTAGHVATGQILNPDAYAHPL---FYRGVDDSTGFR 499
Db 320 ILHGKEDIKVIPTTPADHWALASGLPTTVABESGFTCNIMNASADEMFNFQBGPLDDSGWV 379

Qy 500 TRNIIICPPIKNNRQSVIGVAELVNKINGPWFSEKDEDIATAFSYICGISIAHSLLYKKVN 559
Db 380 IKNVLSMPTVNKKEBIEGVATFYNRKQKPPDDQDEVLMESLTDFLGWSVLNTDTYDKNN 439

Qy 560 BAQYRSHLANEMMYHMKVSDDEYTKLHD-----GIQFVAIDSNFA-----602
Db 440 KLENRKDIAQDMVLVHVRCXDKDEIQEILPTRDLRGKEPADCEEDELGKILKEELPGPTKF 499

Qy 603 ---SFTYTPRSLPREDTSMAILSMLODMNFNNYKIDCPTLARCCLVKKGYRPPPHNW 659
Db 500 DIYEFHFSDBLCTELELVKCKIQMYELGVGVKRFQIQPOEVLVRFVLSVSKAYRRTYHNW 559

Qy 660 MHAFSVSHFCVLLYKNLELTWLEDMELFALFISCMCHDLDRGTNNNSFQVASKSLAAL 719
Db 560 GHGFNVAQTMFTLLMTGKLSYYTDLFAFMVATGLCHDIDHRGTNNLYQMKSNQPLAKL 619

Qy 720 YSSEGSVMRHHFAQAIILNTHGNCNIFDHSRKDYQRMMLDRDIIILATDLAHLHIFPK 779
Db 620 HGS--SILERHHLBFGKFLABESLNIYONLNRQHEHVIHLMDAITATDLALVFKKRT 677
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Qy 780 DLQKWA-----VGVDRTNKQHHSLLLCLMTSCDLSDOTKGMKTKTKRIABLIY 828
Db 678 MFQKIVDESRYEDKKSWVEYLSLETTKEILVMAMMTACDLSALTKEPWEVQSRVALLVA 737

Qy 829 KEFFSQGDLEK-AMGNRPMEHMDREK-AIYELQITSPMEHTAMPIYKLLQDLF 879
Db 738 AEFWEQGDLERTVLDQQPIPMWDRNKAELPKLVQGFIDFVCTFYFKPLGIP 790

RESULT 15
S06418
3',5'-cyclic-GMP phosphodiesterase (EC 3.1.4.35) alpha chain - bovine
N:Alternate names: cGMP phosphodiesterase alpha chain
C:Species: Bos primigenius taurus (cattle)
C:Date: 30-Sep-1993 #sequence_revision 30-Sep-1993 #text_change 09-Jul-2004
C:Accession: S06418; S27007; S00161; A34611; S08516
R:Ovchinnikov, Y.A.; Gubanov, V.V.; Khrantsov, N.V.; Akhmedov, N.B.; Ishchenko, K.A.; Zha
T.M.; Bystron, N.S.; Severtsova, I.V.; Lipkin, V.M.
Dokl. Biochem. 296, 303-307, 1987
A:Title: Cyclic GMP phosphodiesterase from bovine retina. Amino acid sequence of the alp
A:Reference number: S06418
A:Accession: S06418
A:Molecule type: mRNA
A:Residues: 1-859 <OVI>
A:Cross-references: UNIPROT:P11541; EMBL:X12756; NID:g616; PIDN:CAA31243.1; PID:g617
A:Accession: S27007
A:Molecule type: protein
A:Residues: 2-11;22-27;32-40;95-98;112-115;180-193;248-267;275-282;297-306;312-330;361-3
645;654-661;663-667;703-712;734-736;751-760;766-771;787-798;811-819 <OVG>
A:Note: This paper is a translation of the Russian paper published in Dokl. Akad. Nauk S
R:Ovchinnikov, Y.A.; Gubanov, V.V.; Khrantsov, N.V.; Ischenko, K.A.; Zagranichny, V.E.;
FEBS Lett. 223, 169-173, 1987
A:Title: Cyclic GMP phosphodiesterase from bovine retina. Amino acid sequence of the alp
A:Reference number: S00161; MUID:88030033; PMID:2822478
A:Accession: S00161
A:Molecule type: mRNA
A:Residues: 1-859 <OV2>
A:Cross-references: EMBL:M27541; NID:g162826; PIDN:AAA30441.1; PID:g162828
A:Note: part of this sequence was confirmed by protein sequencing
R:Pittler, S.J.; Baehr, W.; Wasemuth, J.J.; McConnell, D.G.; Champagne, M.S.; vanTuinen,
Genomics 6, 272-283, 1990
A:Title: Molecular characterization of human and bovine rod photoreceptor cGMP phosphodi
A:Reference number: A34611; MUID:90169986; PMID:2155175
A:Accession: A34611
A:Molecule type: mRNA
A:Residues: 1-193,'V',195-423,'T',425-674,'P',676-859 <PIT>
A:Cross-references: GB:M26043; NID:g162833; PIDN:AAA30443.1; PID:g162834
C:Comment: This protein is involved in the transduction and amplification of the visual
C:Superfamily: 3',5'-cyclic-GMP phosphodiesterase alpha chain; 3',5'-cyclic-nucleotide
C:Keywords: acetylated amino end; cGMP; heterotrimer; phosphoric diester hydrolase; reti
F:2-859/Product: 3',5'-cyclic-GMP phosphodiesterase alpha chain #status experimental <MA
F:558-791/Domain: 3',5'-cyclic-nucleotide phosphodiesterase homology <CNP>
F:2/Modified site: acetylated amino end (Gly) (in mature form) #status experimental

Query Match      15.3%; Score 753.5; DB 1; Length 859;
Best Local Similarity 26.1%; Pred. No. 1.3e-40;
Matches 217; Conservative 150; Mismatches 349; Indels 115; Gaps 24;

Qy 210 PEEAGDQKGG--GVAYTDQDKILQGLGYD-LDASSLQKLVQYLOQBTQASRCCLLL 266
Db 39 PREAAVDFSNYHALNSVEESEIIFDLRLDFQDNLOAEKCVFNVMKKLCFLQADRMSLFM 98

Qy 267 VSEDN--LQISCKVIG---DKVLEE-----EISFPLTTGRLGQVVEDKKSIOKLQUTS 314
Db 99 YRARGIAELATRLFNHVKDAVLBECLVAPDSEIVFPFLDMGVGVHVALSKIVNVPN-TE 157

Qy 315 ED---MQQLQSMGLGEVQAMLCVPVISRATQOVVALACAFNKLGGDLFTDDEHVIQCHF 371
Db 158 EDEHCFDVPDTLTETBYQKNILASPIMN--GKDVVAIIMAVNKNVDPGPHPTENDEILLKYL 215

Qy 372 HVTSTVLSTLFAQEQKLCCEC---QALLQVAKNLFTHLDDVSVLLQELIITEARNLSNA 428
```



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OM protein - protein search, using sw model

Run on: June 26, 2005, 12:06:11 ; Search time 117.813 Seconds  
(without alignments)  
3092.423 Million cell updates/sec

Title: US-10-697-894-43  
Perfect score: 4911  
Sequence: 1 MGQACGHSILCRSQYPAAR.....VPLDGRAPINGCCSLDAE 942

Scoring table: BLOSUM62  
Gapop 10.0 , Gapext 0.5

Searched: 2105692 seqs, 386760381 residues

Total number of hits satisfying chosen parameters: 2105692

Minimum DB seq length: 0  
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%  
Maximum Match 100%  
Listing first 45 summaries

Database : A\_Geneseq\_16Dec04:\*  
1: Geneseqp1980s:\*  
2: Geneseqp1990s:\*  
3: Geneseqp2000s:\*  
4: Geneseqp2001s:\*  
5: Geneseqp2002s:\*  
6: Geneseqp2003as:\*  
7: Geneseqp2003bs:\*  
8: Geneseqp2004s:\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

#### SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	4911	100.0	942	2	AAR69728 Cyclic-GM
2	4911	100.0	942	2	Aaw11239 Cyclic GM
3	4911	100.0	942	2	Aaw18049 cGS-PDE a
4	4911	100.0	942	2	Aaw71225 Bovine br
5	4911	100.0	942	2	Aaw77041 Cyclic-GM
6	4911	100.0	942	2	Aaw60753 cGS-PDE 1
7	4911	100.0	942	2	Aay80985 Bovine br
8	4911	100.0	942	6	ABU58724 Bovine br
9	4911	100.0	942	8	ADQ94963 Bovine cG
10	4871	99.2	942	2	AAR28408 Cyclic-GM
11	4728.5	96.3	941	2	AAR69729 Cyclic-GM
12	4728.5	96.3	941	2	Aaw11253 pHCgs6n c
13	4728.5	96.3	941	2	Aaw18050 Human cGS
14	4728.5	96.3	941	2	Aaw71226 Human cGS
15	4728.5	96.3	941	2	Aaw77042 Cyclic-GM
16	4728.5	96.3	941	2	Aaw60754 Human cGS
17	4728.5	96.3	941	3	Aay80986 Human cGS
18	4728.5	96.3	941	4	Aae07954 Human pho
19	4728.5	96.3	941	4	Aae07918 Human pho
20	4728.5	96.3	941	4	AAB85117 Human cGM
21	4728.5	96.3	941	4	AAB85106 Human cGM
22	4728.5	96.3	941	4	AAG66539 Human int
23	4728.5	96.3	941	6	ABU58725 Human bra
24	4728.5	96.3	941	7	ADd14154 Human src
25	4728.5	96.3	941	7	ADe62314 Human Pro

26	4728.5	96.3	941	8	ADO21792	Ado21792 Human pho
27	4728.5	96.3	941	8	ADQ94965	Adq94965 Plasmid p
28	4690.5	95.5	941	2	AAR28409	Aar28409 Human foe
29	4657	94.8	921	2	AAR69727	Aar69727 Cyclic-GM
30	4657	94.8	921	2	Aaw11252	Aaw11252 Clone p3C
31	4657	94.8	921	2	Aaw18048	Aaw18048 Cyclic-GM
32	4657	94.8	921	2	Aaw71224	Aaw71224 cGS-PDE e
33	4657	94.8	921	2	Aaw77040	Aaw77040 Adrenal c
34	4657	94.8	921	2	Aaw60752	Aaw60752 cGS-PDE i
35	4657	94.8	921	3	AAY80984	Aay80984 Bovine ad
36	4657	94.8	921	6	ABU58723	Abu58723 Bovine ad
37	4657	94.8	921	8	ADQ94959	Adq94959 Bovine p3
38	4640	94.5	921	2	AAR28407	Aar28407 cGS-PDE f
39	4480.5	91.2	920	6	ABR54205	ABr54205 Human NOV
40	4474.5	91.1	920	5	AAQ15507	AAo15507 Human pho
41	4474.5	91.1	920	5	ABG70998	ABg70998 Human pho
42	4418	90.0	928	7	ADe62312	AdE62312 Rat Prote
43	4272.5	87.0	950	7	ADM04243	Adm04243 Human pro
44	3484.5	71.0	786	7	ADB64790	ADB64790 Human pro
45	3345	68.1	685	8	ADR10446	ADR10446 Human pro

#### ALIGNMENTS

RESULT 1  
AAR69728  
ID AAR69728 standard; protein; 942 AA.  
XX AC AAR69728;  
XX DT 25-MAR-2003 (revised)  
DT 11-OCT-1995 (first entry)  
XX DE Cyclic-GMP stimulated nucleotide PDE clone pBBCGSPDE-7.  
XX KW Cyclic-GMP stimulated nucleotide phospho-diesterase; antibodies;  
KW bovine adrenal cortex; hormones; neurotransmitters;  
KW transmission regulation; enzyme purification; clone pBBCGSPDE-7.  
XX OS Bos taurus.  
XX PN US5389527-A.  
XX PD 14-FEB-1995.  
XX PF 20-APR-1992; 92US-00872644.  
XX PR 19-APR-1991; 91US-00688356.  
XX PA (UNIW ) UNIV WASHINGTON.  
XX PI Sonnenburg WK, Charbonneau H, Beavo JA;  
XX DR WPI; 1995-090205/12.  
XX PS N-PSDB; AAQ83977.  
XX PT New nucleic acid encoding cyclic-GMP stimulated nucleotide phospho-  
PT diesterase \_ and related vectors and transformed cells, useful for  
PT screening cpds. for phospho-di:esterase modulating activity.  
XX Example 5; Col 79-86; 69pp; English.  
XX CC AAQ83977 encodes AAR69728 the bovine brain cyclic-GMP stimulated  
CC nucleotide phospho-diesterase (Cam PDE) clone pBBCGSPDE-7. Eukaryotic  
CC cells that express Cam PDE can be used to screen cpds. for the ability to  
CC modulate Cam PDE activity. Cam PDEs are involved in regulating the  
CC transmission of information from hormones, neurotransmitters or other  
CC systems that use cyclic nucleotides as messengers. Antibodies raised  
CC against Cam PDE can be used for enzyme purificn., or determination.  
XX (Updated on 25-MAR-2003 to correct PF field.)  
XX Sequence 942 AA;

Query Match	100.0%;	Score 4911;	DB 2;	Length 942;
Best Local Similarity	100.0%;	Pred. No. 0;		
Matches 942;	Conservative 0;	Mismatches 0;	Indels 0;	Gaps 0;
QY	1	MGQACGHSILCRSQYPAARPAERGGQVFLKPDPEPPPPPCADSLQDALLSLGSDIVD	60	
DB	1	MGQACGHSILCRSQYPAARPAERGGQVFLKPDPEPPPPPCADSLQDALLSLGSDIVD	60	
QY	61	AGLOAVKEALSAVLPKVTYTYLLDGSRLVCEPPHELPOBQKREAVISRRLGCN	120	
DB	61	AGLOAVKEALSAVLPKVTYTYLLDGSRLVCEPPHELPOBQKREAVISRRLGCN	120	
QY	121	GLGPSDLPGKPLARLAPLAPDQVLPVLDKEAGAAVILVHCQGLSNEEWSLOAV	180	
DB	121	GLGPSDLPGKPLARLAPLAPDQVLPVLDKEAGAAVILVHCQGLSNEEWSLOAV	180	
QY	181	EKHTLVALKRVQALQORESSVAPEATQNPPEAAGDQGGVAYTDQDRKILQLCGELYDL	240	
DB	181	EKHTLVALKRVQALQORESSVAPEATQNPPEAAGDQGGVAYTDQDRKILQLCGELYDL	240	
QY	241	DASSLQLKVLQYLOQETQASRCCLLLVSEDNLQLSCKVIGDKVLEBESFPPLTTGRIGQV	300	
DB	241	DASSLQLKVLQYLOQETQASRCCLLLVSEDNLQLSCKVIGDKVLEBESFPPLTTGRIGQV	300	
QY	301	VEDKKSICQLDTSQDMOQSLGCEVQMLCVPVISRATDQVVALACAFKLGGLDFT	360	
DB	301	VEDKKSICQLDTSQDMOQSLGCEVQMLCVPVISRATDQVVALACAFKLGGLDFT	360	
QY	361	DQDEHVIQCHFYHTSVLTSTLAFQEQKLCCEQALLQVAKNLFTHLDDVSVLLQEIT	420	
DB	361	DQDEHVIQCHFYHTSVLTSTLAFQEQKLCCEQALLQVAKNLFTHLDDVSVLLQEIT	420	
QY	421	EARNLSNAEICSVFLLDQNELVAKVDFGQVVEDESYEIRIPADQGIAGHVATTGQILNIP	480	
DB	421	EARNLSNAEICSVFLLDQNELVAKVDFGQVVEDESYEIRIPADQGIAGHVATTGQILNIP	480	
QY	481	DAYAHLFVRGVDDSTGRFTRNLCPPIKNEQEVIGVAELVKNKINGPWFSEKEDLATA	540	
DB	481	DAYAHLFVRGVDDSTGRFTRNLCPPIKNEQEVIGVAELVKNKINGPWFSEKEDLATA	540	
QY	541	FSIYCGISIAHSLLYKKNVNEAQYRSHLANEMMYHMKVSDDEYTKLLHDGIGQVAAIDSN	600	
DB	541	FSIYCGISIAHSLLYKKNVNEAQYRSHLANEMMYHMKVSDDEYTKLLHDGIGQVAAIDSN	600	
QY	601	PASFTYTPRSPEDDTSMALLSMLQDMFNINNYKIDCPTLARFCLMVKKGYRDPYHNWM	660	
DB	601	PASFTYTPRSPEDDTSMALLSMLQDMFNINNYKIDCPTLARFCLMVKKGYRDPYHNWM	660	
QY	661	HAFSVSHFCYLLYKNLENTYLEDMEIFALFISCMCHDLHRTGNTNSFQVASKSVLAALY	720	
DB	661	HAFSVSHFCYLLYKNLENTYLEDMEIFALFISCMCHDLHRTGNTNSFQVASKSVLAALY	720	
QY	721	SSEGSVMERHFAQAIALINTHGCNIFDHFSSKDYQRMMLDMRDIIILATDLAHLRIFKD	780	
DB	721	SSEGSVMERHFAQAIALINTHGCNIFDHFSSKDYQRMMLDMRDIIILATDLAHLRIFKD	780	
QY	781	LQKMAEVGYDRNTKQHSLLCLLMTSCDLSQTKGWTTRKIAELIYKEFPFSGDLEKA	840	
DB	781	LQKMAEVGYDRNTKQHSLLCLLMTSCDLSQTKGWTTRKIAELIYKEFPFSGDLEKA	840	
QY	841	MGNRPMEMMDREKAVIPELOISFMEHIAMPYIKLLQDLFPKAAELYERVASNRHWTKVS	900	
DB	841	MGNRPMEMMDREKAVIPELOISFMEHIAMPYIKLLQDLFPKAAELYERVASNRHWTKVS	900	
QY	901	HKFTIRGLPSNNSLDFDEEVEVPLDGRAPINGCCSLDAE	942	
DB	901	HKFTIRGLPSNNSLDFDEEVEVPLDGRAPINGCCSLDAE	942	

RESULT 2  
AAW11239  
ID AAW11239 standard; protein; 942 AA.

XX	AAW11239;
AC	
XX	25-MAR-2003 (revised)
DT	17-MAR-1997 (first entry)
DT	
XX	Cyclic GMP stimulated phosphodiesterase.
XX	
XX	Cyclic GMP stimulated phosphodiesterase; cGS-PDE; bovine; brain; cAMP;
KW	adrenal gland; cGMP; transmembrane signal; extracellular hormone;
KW	neurotransmitter; antibody.
XX	
OS	Bos taurus.
XX	
XX	US5580771-A.
XX	
PD	03-DEC-1996.
XX	
XX	29-AUG-1994; 94US-00297494.
PP	
PP	19-APR-1991; 91US-00688356.
PR	20-APR-1992; 92US-00872644.
XX	
XX	(UNIW ) UNIV WASHINGTON.
XX	
PI	Charbonneau H, Sonnenburg WK, Beavo JA;
XX	
DR	WPI; 1997-033573/03.
DR	N-PSDB; AAT51090.
XX	DNA encoding cGMP-stimulated phosphodiesterase - for prodn. of
PT	recombinant enzyme.
PT	
XX	Claim 1; Col 77-86; 68pp; English.
PS	
XX	This sequence represents the cyclic GMP stimulated phosphodiesterase (cGS
CC	-PDE) clone PBBCSPDE-5 isolated from bovine brain. This sequence is
CC	nearly identical to the bovine adrenal gland cGS-PDE isozyme. The cyclic
CC	nucleotide phosphodiesterases (PDEs) catalyze the hydrolysis of 3',5'
CC	cyclic nucleotides, such as cAMP and cGMP, to their corresponding 5'-
CC	nucleotide monophosphates. The PDEs are therefore important in the
CC	control of the cellular concentration of cyclic nucleotides. The PDEs
CC	are, in turn, regulated by transmembrane signals or second messenger
CC	ligands such as calcium ion or cGMP. The PDEs therefore have a central
CC	role in regulating the flow of information from extracellular hormones,
CC	neurotransmitters, or other signals that use the cyclic nucleotides as
CC	messengers. PDEs are present in most of the cells and tissues of
CC	eukaryotic organisms, but only in trace amounts. cGS-PDEs are stimulated
CC	by cGMP in effecting cAMP hydrolysis. This is thought to occur through a
CC	noncatalytic cGMP-specific site present on the cGS-PDE. The DNA encoding
CC	this sequence can be used for the production of recombinant cGS-PDE,
CC	which may have therapeutic and diagnostic uses. This sequence may also be
CC	useful for diagnostic antibody production. (Updated on 25-MAR-2003 to
CC	correct PF field.)
XX	
SQ	Sequence 942 AA;

Query Match	100.0%;	Score 4911;	DB 2;	Length 942;
Best Local Similarity	100.0%;	Pred. No. 0;		
Matches 942;	Conservative 0;	Mismatches 0;	Indels 0;	Gaps 0;
QY	1	MGQACGHSILCRSQYPAARPAERGGQVFLKPDPEPPPPPCADSLQDALLSLGSDIVD	60	
DB	1	MGQACGHSILCRSQYPAARPAERGGQVFLKPDPEPPPPPCADSLQDALLSLGSDIVD	60	
QY	61	AGLOAVKEALSAVLPKVTYTYLLDGSRLVCEPPHELPOBQKREAVISRRLGCN	120	
DB	61	AGLOAVKEALSAVLPKVTYTYLLDGSRLVCEPPHELPOBQKREAVISRRLGCN	120	
QY	121	GLGPSDLPGKPLARLAPLAPDQVLPVLDKEAGAAVILVHCQGLSNEEWSLOAV	180	
DB	121	GLGPSDLPGKPLARLAPLAPDQVLPVLDKEAGAAVILVHCQGLSNEEWSLOAV	180	

```
QY 181 EKHTLVALKRVQALQOQRESSVAPEATQNPPEEAAAGQKGGVAYTDDQDKILQLCGELYDL 240
DB 181 EKHTLVALKRVQALQOQRESSVAPEATQNPPEEAAAGQKGGVAYTDDQDKILQLCGELYDL 240
QY 241 DASSLQLKVLQYLOQETOASRCCLLVSDNLQSKVIGDKVLEEEISFPLTTGRLGV 300
DB 241 DASSLQLKVLQYLOQETOASRCCLLVSDNLQSKVIGDKVLEEEISFPLTTGRLGV 300
QY 301 VEDKKSILQKDLTSEDMDQQLQSMGCEVQAMLCVPVISRATDQVVALACAFNKLGGDLFT 360
DB 301 VEDKKSILQKDLTSEDMDQQLQSMGCEVQAMLCVPVISRATDQVVALACAFNKLGGDLFT 360
QY 361 DQDEHVIQHCFTHTSTLTSTLAFQKEQKLKCECQALLQVAKNLFTHLDDVSVLQEIIT 420
DB 361 DQDEHVIQHCFTHTSTLTSTLAFQKEQKLKCECQALLQVAKNLFTHLDDVSVLQEIIT 420
QY 421 EARNLSNAEICSVFLLDQNELVAKVFDGGVVEDESEYIRIPADQGIAGHVATTGQILNIP 480
DB 421 EARNLSNAEICSVFLLDQNELVAKVFDGGVVEDESEYIRIPADQGIAGHVATTGQILNIP 480
QY 481 DAYAHPFLFYRGVDDSTGFRTRNLCFPIKNENQEVIGVAELVNKINGPWFSEDEDLATA 540
DB 481 DAYAHPFLFYRGVDDSTGFRTRNLCFPIKNENQEVIGVAELVNKINGPWFSEDEDLATA 540
QY 541 FSIYCGISIAHSLLYKKVNEAQYRSHLANEMMYHMKVSDDEYTKLLHDGIQPVAAIDSN 600
DB 541 FSIYCGISIAHSLLYKKVNEAQYRSHLANEMMYHMKVSDDEYTKLLHDGIQPVAAIDSN 600
QY 601 PASFTYTPRSLPDDDTSMALLSMLQDMNFNNYKIDCPTLARFCMLVKKGYRDPVYHNM 660
DB 601 PASFTYTPRSLPDDDTSMALLSMLQDMNFNNYKIDCPTLARFCMLVKKGYRDPVYHNM 660
QY 661 HAFSVSHFCYLLKYLENTYLEDMEIFALFISCMCHDLDRGTNNNSFOVASKSVLAALY 720
DB 661 HAFSVSHFCYLLKYLENTYLEDMEIFALFISCMCHDLDRGTNNNSFOVASKSVLAALY 720
QY 721 SSEGSMERHHPAQAIATLNTGNCNIFDHFSTRKYQYRMDLMDRIILATDLAHLRIKPD 780
DB 721 SSEGSMERHHPAQAIATLNTGNCNIFDHFSTRKYQYRMDLMDRIILATDLAHLRIKPD 780
QY 781 LQKMAEYGYDRTNKQHSLLCLLMTSCDLSDQTKGKTKTRIAELIYKEFFSQGDLEKA 840
DB 781 LQKMAEYGYDRTNKQHSLLCLLMTSCDLSDQTKGKTKTRIAELIYKEFFSQGDLEKA 840
QY 841 MGNRRPMEHMDREKAYIPELQISFMEHIAMPIYKLLQDLFPKAAELYERVASNRHWTKVS 900
DB 841 MGNRRPMEHMDREKAYIPELQISFMEHIAMPIYKLLQDLFPKAAELYERVASNRHWTKVS 900
QY 901 HKFTIRGLPSNNSLDPLDEYEVDPDLDGARAPINGCCSLDAE 942
DB 901 HKFTIRGLPSNNSLDPLDEYEVDPDLDGARAPINGCCSLDAE 942
```

## RESULT 3

```
AAW18049
ID AAW18049 standard; protein; 942 AA.
XX
AC AAW18049;
XX
DT 25-MAR-2003 (revised)
DT 05-AUG-1997 (first entry)
```

XX CGS-PDE amino acid sequence from the pBBCSPDE-7 insert.

XX Cyclic-GMP-stimulated phosphodiesterase; antibody; cow;

KW polymerase chain reaction.

XX Bos taurus.

XX US5602019-A.

XX 11-FEB-1997.

XX

PF 29-AUG-1994; 94US-00297510.

XX

PR 19-APR-1991; 91US-00688356.

XX

PR 20-APR-1992; 92US-00872644.

XX

PA (UNIW ) UNIV WASHINGTON.

XX

PI Sonnenburg WK, Charbonneau H, Bentley JK, Beavo JA;

XX

DR WPI; 1997-131799/12.

XX

DR N-PSDB; AAT67223.

XX

PT DNA encoding bovine and human phosphodiesterase enzymes - stimulated by

XX

PT calcium/calmodulin, useful for recombinant prodn. of the enzymes.

XX

PS Example 5; Col 85-92; 69pp; English.

XX

CC The present sequence represents the pBBCSPDE-7 bovine brain insert amino

XX

CC acid sequence. The large open reading frame encodes a 942-residue

XX

CC polypeptide that is nearly identical to the adrenal gland cyclic-GMP-

XX

CC stimulated phosphodiesterase (CGS-PDE) isozyme. The difference in the

XX

CC primary structure of the two isozymes lies in the amino-terminal residues

XX

CC 1-46 of the brain CGS-PDE, and residues 1-25 of the adrenal CGS-PDE. The

XX

CC remaining carboxy-terminal residues in both are identical. The DNA

XX

CC sequences of the CGS-PDE's are used for the production of the recombinant

XX

CC enzymes, which in turn may be used for antibody production and to screen

XX

CC for compounds that modulate phosphodiesterase activity. (Updated on 25-

XX

CC MAR-2003 to correct Pf field.) (Updated on 25-MAR-2003 to correct Pf

XX

CC field.)

XX

SQ Sequence 942 AA;

Query Match 100.0%; Score 4911; DB 2; Length 942;

Best Local Similarity 100.0%; Pred. No. 0;

Matches 942; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 MQQACGHSILCSQQYPAARPAEPRGQQVFLKPDPPPPPPPCADSLQALLSLGSLVIDV 60

DB 1 MQQACGHSILCSQQYPAARPAEPRGQQVFLKPDPPPPPPPCADSLQALLSLGSLVIDV 60

QY 61 AGLOQAVKEALSAPLKVETVYTYLLDGSRLVCEPPHELPOEGKVRSAVSRKRLGN 120

DB 61 AGLOQAVKEALSAPLKVETVYTYLLDGSRLVCEPPHELPOEGKVRSAVSRKRLGN 120

QY 121 GLGPSDLPGKPLARLAPLAPDQVLPVLDKEAGAAVAALVHVCGLSDNEEWSLQAV 180

DB 121 GLGPSDLPGKPLARLAPLAPDQVLPVLDKEAGAAVAALVHVCGLSDNEEWSLQAV 180

QY 181 EKHTLVALKRVQALQOQRESSVAPEATQNPPEEAAAGQKGGVAYTDDQDKILQLCGELYDL 240

DB 181 EKHTLVALKRVQALQOQRESSVAPEATQNPPEEAAAGQKGGVAYTDDQDKILQLCGELYDL 240

QY 241 DASSLQLKVLQYLOQETOASRCCLLVSDNLQSKVIGDKVLEEEISFPLTTGRLGV 300

DB 241 DASSLQLKVLQYLOQETOASRCCLLVSDNLQSKVIGDKVLEEEISFPLTTGRLGV 300

QY 301 VEDKKSILQKDLTSEDMDQQLQSMGCEVQAMLCVPVISRATDQVVALACAFNKLGGDLFT 360

DB 301 VEDKKSILQKDLTSEDMDQQLQSMGCEVQAMLCVPVISRATDQVVALACAFNKLGGDLFT 360

QY 361 DQDEHVIQHCFTHTSTLTSTLAFQKEQKLKCECQALLQVAKNLFTHLDDVSVLQEIIT 420

DB 361 DQDEHVIQHCFTHTSTLTSTLAFQKEQKLKCECQALLQVAKNLFTHLDDVSVLQEIIT 420

QY 421 EARNLSNAEICSVFLLDQNELVAKVFDGGVVEDESEYIRIPADQGIAGHVATTGQILNIP 480

DB 421 EARNLSNAEICSVFLLDQNELVAKVFDGGVVEDESEYIRIPADQGIAGHVATTGQILNIP 480

QY 481 DAYAHPFLFYRGVDDSTGFRTRNLCFPIKNENQEVIGVAELVNKINGPWFSEDEDLATA 540

DB 481 DAYAHPFLFYRGVDDSTGFRTRNLCFPIKNENQEVIGVAELVNKINGPWFSEDEDLATA 540

QY 541 FSIYCGISIAHSLLYKKVNEAQYRSHLANEMMYHMKVSDDEYTKLLHDGIQPVAAIDSN 600

541 FSIYCGISIAHSLLYKKVNEAQRSHLANEMMYHMKVSDDEYTKLHDLGQPVAAIDSN 600  
 601 FASFTYTPRSLPEDDTSMAILSMLQDMNFNNYKIDCPTLARFCLMWKGYRDPYHNMW 660  
 601 FASFTYTPRSLPEDDTSMAILSMLQDMNFNNYKIDCPTLARFCLMWKGYRDPYHNMW 660  
 661 HAFSVSHFCYLLYKNLELTNYLEDMEIFALFTSCMCHDLDRGTNNSFQVASKSVLAALY 720  
 661 HAFSVSHFCYLLYKNLELTNYLEDMEIFALFTSCMCHDLDRGTNNSFQVASKSVLAALY 720  
 721 SSEGSMVERHFAQAIAIALNTHGNCIFDHFSRKDYQRMQLDMRDIIILATDLAHLRIKPD 780  
 721 SSEGSMVERHFAQAIAIALNTHGNCIFDHFSRKDYQRMQLDMRDIIILATDLAHLRIKPD 780  
 781 LQKMAEYGYDRTNKQHSLLILCLMTSCDLSQDTKGWTKTKIAELIYKEFFSQGDLEKA 840  
 781 LQKMAEYGYDRTNKQHSLLILCLMTSCDLSQDTKGWTKTKIAELIYKEFFSQGDLEKA 840  
 841 MGNRPMEMMDREKAYIPELQISFMEHIAMPIYKLLQDLFPKAAELYERVASNRHHTWTKVS 900  
 841 MGNRPMEMMDREKAYIPELQISFMEHIAMPIYKLLQDLFPKAAELYERVASNRHHTWTKVS 900  
 901 HKFTIRGLPSNNSLDFLDEEYVDPDLCARAPINGCCSLDAE 942  
 901 HKFTIRGLPSNNSLDFLDEEYVDPDLCARAPINGCCSLDAE 942

## RESULT 4

AA711225  
 ID AA711225 standard; protein; 942 AA.  
 XX  
 AC AA711225;  
 XX  
 DT 29-OCT-1998 (first entry)  
 XX  
 DE Bovine brain CGS-PDE sequence of clone pBBCGSPDE-7.  
 XX  
 KW Ca2+/calmodulin sensitive cyclic nucleotide phosphodiesterase; Cam-PDE;  
 KW assay; identification; modification; enzymatic activity; modulator;  
 KW cyclic guanosine monophosphate-stimulated phosphodiesterase; CGS-PDE.

## Bos sp.

XX  
 XX US5800987-A.  
 XX  
 PD 01-SEP-1998.  
 XX  
 PF 31-MAY-1995; 95US-00455525.  
 XX  
 PR 19-APR-1991; 91US-00688356.  
 PR 20-APR-1992; 92US-00872644.  
 PR 29-AUG-1994; 94US-00297494.  
 XX  
 PA (UNIW ) UNIV WASHINGTON.

XX Sonnenburg WK, Charbonneau H, Beavo JA, Bentley JK;

XX WPI; 1998-494762/42.

XX Identification of modulators of Calcium/calmodulin sensitive cyclic  
 PT nucleotide phosphodiesterase - uses recombinant cells expressing the  
 PT enzyme and monitoring protein expression in the presence of potential  
 PT modulators.

XX Example 5; Col 85-90; 69pp; English.

XX The present sequence is encoded by the DNA sequence of clone pBBCGSPDE-7,  
 CC isolated from bovine brain. This clone encodes cyclic guanosine  
 CC monophosphate-stimulated phosphodiesterase (CGS-PDE) cDNA. The  
 CC specification also describes Ca2+/calmodulin sensitive cyclic nucleotide  
 CC phosphodiesterase (Cam-PDE) enzymes. Cam-PDE enzymes catalyze the  
 CC hydrolysis of cyclic nucleotides and as such control their intracellular

CC level. They are controlled by second messengers e.g. Ca2+ and calmodulin  
 CC and transmembrane signals and through pathways involving these, regulate  
 CC flow of information from extracellular hormones, neurotransmitters and  
 CC other signals using cyclic nucleotides as messengers. The specification  
 CC describes an assay for identifying a chemical agent which modifies the  
 CC enzymatic activity of a mammalian Cam-PDE. The assays are useful for  
 CC identifying modulators of Cam-PDEs. The assay is carried out by  
 CC incubating cells expressing Cam-PDE with the suspected modulator and  
 CC measuring its effect e.g. monitoring the hydrolysis of cAMP and/or CGMP  
 XX

SQ Sequence 942 AA;

Query Match 100.0%; Score 4911; DB 2; Length 942;  
 Best Local Similarity 100.0%; Pred. No. 0;  
 Matches 942; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
 Qy 1 MQQACGSHILCRSQQYPAARPAEPGRQQVFLKPBDEPPPPQPCADSLQDALLSLGSDIV 60  
 Db 1 MQQACGSHILCRSQQYPAARPAEPGRQQVFLKPBDEPPPPQPCADSLQDALLSLGSDIV 60  
 Qy 61 AGLOQAVKEALSAVLPKVTETVYLLDGESRLVCEEPPELPOEGKVEAVISRKLGCN 120  
 Db 61 AGLOQAVKEALSAVLPKVTETVYLLDGESRLVCEEPPELPOEGKVEAVISRKLGCN 120  
 Qy 121 GLGPSDLPGKPLARLVAAPDQVLPVLDKEAGAAVAVILVHCQGLSDNEEWSLOAV 180  
 Db 121 GLGPSDLPGKPLARLVAAPDQVLPVLDKEAGAAVAVILVHCQGLSDNEEWSLOAV 180  
 Qy 181 EKHTLVALKRVQALQORESSVAPEATQNPPEAAGDQKGVAYTDQDRKILQLCGELYDL 240  
 Db 181 EKHTLVALKRVQALQORESSVAPEATQNPPEAAGDQKGVAYTDQDRKILQLCGELYDL 240  
 Qy 241 DASSLQLKVLQYLOQETQASRCCLLVSEDNLQLSCKVIGDKVLEEEISPLTTGRLQGV 300  
 Db 241 DASSLQLKVLQYLOQETQASRCCLLVSEDNLQLSCKVIGDKVLEEEISPLTTGRLQGV 300  
 Qy 301 VEDKKSITQLKDLTSEDMMQQLQSMGCEVQAMLCVPVISRATDQVVALACAFKLGDLFT 360  
 Db 301 VEDKKSITQLKDLTSEDMMQQLQSMGCEVQAMLCVPVISRATDQVVALACAFKLGDLFT 360  
 Qy 361 DQDESHVIOHCFHYTSTVLTSTLAFQKQKQKCECOALLQVAKNLFTHLDDVSVLLQEIIT 420  
 Db 361 DQDESHVIOHCFHYTSTVLTSTLAFQKQKQKCECOALLQVAKNLFTHLDDVSVLLQEIIT 420  
 Qy 421 EARNLSNAEITCSVELLDONELVAKVFDGGVVEDESYEIRIPADQGIAGHVATTGQILNIP 480  
 Db 421 EARNLSNAEITCSVELLDONELVAKVFDGGVVEDESYEIRIPADQGIAGHVATTGQILNIP 480  
 Qy 481 DAYAHPLYRGVDDSTGFRTRNLCFPIKNEHQEVIQVAELVNKINGPWFSKFDBDLATA 540  
 Db 481 DAYAHPLYRGVDDSTGFRTRNLCFPIKNEHQEVIQVAELVNKINGPWFSKFDBDLATA 540  
 Qy 541 FSIYCGISIAHSLLYKKVNEAQRSHLANEMMYHMKVSDDEYTKLHDLGQPVAAIDSN 600  
 Db 541 FSIYCGISIAHSLLYKKVNEAQRSHLANEMMYHMKVSDDEYTKLHDLGQPVAAIDSN 600  
 Qy 601 FASFTYTPRSLPEDDTSMAILSMLQDMNFNNYKIDCPTLARFCLMWKGYRDPYHNMW 660  
 Db 601 FASFTYTPRSLPEDDTSMAILSMLQDMNFNNYKIDCPTLARFCLMWKGYRDPYHNMW 660  
 Qy 661 HAFSVSHFCYLLYKNLELTNYLEDMEIFALFTSCMCHDLDRGTNNSFQVASKSVLAALY 720  
 Db 661 HAFSVSHFCYLLYKNLELTNYLEDMEIFALFTSCMCHDLDRGTNNSFQVASKSVLAALY 720  
 Qy 721 SSEGSMVERHFAQAIAIALNTHGNCIFDHFSRKDYQRMQLDMRDIIILATDLAHLRIKPD 780  
 Db 721 SSEGSMVERHFAQAIAIALNTHGNCIFDHFSRKDYQRMQLDMRDIIILATDLAHLRIKPD 780  
 Qy 781 LQKMAEYGYDRTNKQHSLLILCLMTSCDLSQDTKGWTKTKIAELIYKEFFSQGDLEKA 840  
 Db 781 LQKMAEYGYDRTNKQHSLLILCLMTSCDLSQDTKGWTKTKIAELIYKEFFSQGDLEKA 840  
 Qy 841 MGNRPMEMMDREKAYIPELQISFMEHIAMPIYKLLQDLFPKAAELYERVASNRHHTWTKVS 900

Db 841 MGNRPMMMDREKAYIPQLQISFMEHIAPIYKLLQDLFPKAAELVRSNREHWTKVS 900  
AAW77041  
QY 901 HKFTIRGLPSNNSLDPLDEBEYEPDLDGARAPINGCCSLDAE 942  
Db 901 HKFTIRGLPSNNSLDPLDEBEYEPDLDGARAPINGCCSLDAE 942  
RESULT 5  
AAW77041  
ID AAW77041 standard; protein; 942 AA.  
XX  
AC AAW77041;  
XX  
DT 09-NOV-1998 (first entry)  
XX  
DE Cyclic-GMP-stimulated phosphodiesterase clone pBBCGSPDE-7.  
XX  
KW Cow; Ca2+ stimulated phosphodiesterase;  
KW Calmodulin stimulated phosphodiesterase; therapeutic; antibody.  
XX  
OS Bos sp.  
XX  
XX US5789553-A.  
XX  
XX 04-AUG-1998.  
XX  
XX 31-MAY-1995; 95US-00455526.  
XX  
XX 19-APR-1991; 91US-00688356.  
XX  
XX 20-APR-1992; 92US-00872644.  
XX  
XX 29-AUG-1994; 94US-00297494.  
XX  
XX (UNIW ) UNIV WASHINGTON.  
XX  
XX Sonnenburg WK, Charbonneau H, Beavo JA, Bentley JK;  
XX  
XX WPI; 1998-446185/38.  
XX  
XX N-PSDB; AAV48204.  
XX  
XX Antibody to phosphodiesterase polypeptide - useful for purification or  
XX detection of polypeptide.  
XX  
XX Example 5; Column 77/86; 68pp; English.  
XX  
XX The cyclic-GMP-stimulated phosphodiesterase clone pBBCGSPDE-7 from the  
XX bovine brain, is one of several phosphodiesterases isolated in this  
XX invention. The phosphodiesterases were used to transform host cells,  
XX preferably mammalian or yeast cells. The recombinant proteins and  
XX fragments produced can be used for therapeutic, diagnostic, and  
XX prognostic purposes and will provide the basis for preparation of  
XX monoclonal and polyclonal antibodies. An antibody specific for the  
XX Ca2+/calmodulin-stimulated cyclic nucleotide phosphodiesterase (PDE)  
XX polypeptide is useful for affinity purification or detection of the  
XX polypeptide and is selective only for the Ca2+/calmodulin stimulated  
XX cyclic nucleotide PDE polypeptide  
XX  
SQ Sequence 942 AA;  
Query Match 100.0%; Score 4911; DB 2; Length 942;  
Best Local Similarity 100.0%; Pred. No. 0;  
Matches 942; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
QY 1 MQQAGCHSLTCSRQQYPAARPAEPGRQQVFLKPDPPPPPPQPCADSLQDALLSLGSVIDV 60  
Db 1 MQQAGCHSLTCSRQQYPAARPAEPGRQQVFLKPDPPPPPPQPCADSLQDALLSLGSVIDV 60  
QY 61 AGLQAVKEALSAPLKPVTYVTVYLLDGSRLVCEBPPELPHQEGKVRVAVISRRLGCN 120  
Db 61 AGLQAVKEALSAPLKPVTYVTVYLLDGSRLVCEBPPELPHQEGKVRVAVISRRLGCN 120  
QY 121 GLGPSDLPGKPLARLVAPLAPDTQVLVPLVDKEAGAAVAVILVHCGQLSDNEWSLQAV 180

Db 121 GLGPSDLPGKPLARLVAPLAPDTQVLVPLVDKEAGAAVAVILVHCGQLSDNEWSLQAV 180  
QY 181 EXHTLVALKRVQALQORESSVAPEATQNPPEAAGQKGGVAYTTDQDKILQLCGELYDL 240  
Db 181 EXHTLVALKRVQALQORESSVAPEATQNPPEAAGQKGGVAYTTDQDKILQLCGELYDL 240  
QY 241 DASSLQLKVLQYLOQETQASRCCLLLVSDNQLQSCVKVIGDKVLEEEISFPLTTGRLGV 300  
Db 241 DASSLQLKVLQYLOQETQASRCCLLLVSDNQLQSCVKVIGDKVLEEEISFPLTTGRLGV 300  
QY 301 VEDKKSIOQLKDLTSDMQMLGCEVQAMLCVPISRATQOVVALACAFNKLGGDLFT 360  
Db 301 VEDKKSIOQLKDLTSDMQMLGCEVQAMLCVPISRATQOVVALACAFNKLGGDLFT 360  
QY 361 DQDEHVIQHCFTYTSVLTSTLAFQKEQKLCCEQALLQVAKNLFTHLDDVSVLLQEIT 420  
Db 361 DQDEHVIQHCFTYTSVLTSTLAFQKEQKLCCEQALLQVAKNLFTHLDDVSVLLQEIT 420  
QY 421 EARNLSNAEICSVFLLDQNELVAKVFDGGVDESEYEIRIPADQGIAGHVATTGQILNIP 480  
Db 421 EARNLSNAEICSVFLLDQNELVAKVFDGGVDESEYEIRIPADQGIAGHVATTGQILNIP 480  
QY 481 DAYAHPLFYRGVDDSTGPRTRNLCFPIKNENQEVIGVAVELVKNKINGPWFSPDEDLATA 540  
Db 481 DAYAHPLFYRGVDDSTGPRTRNLCFPIKNENQEVIGVAVELVKNKINGPWFSPDEDLATA 540  
QY 541 FSIYCGISIAHSLLYKKVNEAQYRSHLANEMMYHMKVSDDEYTKLLHDGQIPVAAIDSN 600  
Db 541 FSIYCGISIAHSLLYKKVNEAQYRSHLANEMMYHMKVSDDEYTKLLHDGQIPVAAIDSN 600  
QY 601 PASFTYTPRSLPEDDTSMALLSNLQDMNFNNYKIDCPTLARFCLMVKGYRDPPTNNWM 660  
Db 601 PASFTYTPRSLPEDDTSMALLSNLQDMNFNNYKIDCPTLARFCLMVKGYRDPPTNNWM 660  
QY 661 HAFVSVSHFCYLLYKNLELTNYLEDMEIPALFISCMCHDLDRGTNNNSFOVASKSVLAALY 720  
Db 661 HAFVSVSHFCYLLYKNLELTNYLEDMEIPALFISCMCHDLDRGTNNNSFOVASKSVLAALY 720  
QY 721 SSEGSMERHHPAQAIILNTHGCNIFDHFSRKYQRMLDLMDRIILATDLAHLRIFKD 780  
Db 721 SSEGSMERHHPAQAIILNTHGCNIFDHFSRKYQRMLDLMDRIILATDLAHLRIFKD 780  
QY 781 LQKMAEVGYDRNTKQHSLLCLMTSCDLSQDTGKWTTRKIAELIYKEFFSQGDLKA 840  
Db 781 LQKMAEVGYDRNTKQHSLLCLMTSCDLSQDTGKWTTRKIAELIYKEFFSQGDLKA 840  
QY 841 MGNRPMMMDREKAYIPQLQISFMEHIAPIYKLLQDLFPKAAELVRSNREHWTKVS 900  
Db 841 MGNRPMMMDREKAYIPQLQISFMEHIAPIYKLLQDLFPKAAELVRSNREHWTKVS 900  
QY 901 HKFTIRGLPSNNSLDPLDEBEYEPDLDGARAPINGCCSLDAE 942  
Db 901 HKFTIRGLPSNNSLDPLDEBEYEPDLDGARAPINGCCSLDAE 942  
RESULT 6  
AAW60753  
ID AAW60753 standard; protein; 942 AA.  
XX  
AC AAW60753;  
XX  
DT 07-SEP-1998 (first entry)  
XX  
XX CGS-PDE isolated from bovine brain.  
XX  
XX Bovine; decrease; intracellular concentration; CAMP; cGMP;  
KW calcium ion/calmodulin stimulated cyclic nucleotide phosphodiesterase;  
KW CaM-PDE; therapy; prognosis; diagnosis; specific modulator;  
KW CaM-PDE activity; identification; signalling; extracellular hormone;  
KW neurotransmitter; selective inhibitor; cardiotonic; antidiuretic;  
KW antihypertensive; antithrombotic agent; cGMS-PDE.  
XX cyclic-GMP-nucleotide phosphodiesterase; CGS-PDE.  
XX

OS Bos sp.  
 XX US5776752-A.  
 XX  
 XX  
 XX PD 07-JUL-1998.  
 XX PF 07-JUN-1995; 95US-00479532.  
 XX PR 19-APR-1991; 91US-00688356.  
 XX PR 20-APR-1992; 92US-00872644.  
 XX PR 29-AUG-1994; 94US-00297494.  
 XX  
 XX PA (UNIW ) UNIV WASHINGTON.  
 XX  
 XX Sonnenburg WK, Charbonneau H, Bentley JK, Beavo JA;  
 XX  
 XX WPI; 1998-398038/34.  
 XX DR N-PSDB; AAV36156.  
 XX  
 XX New calmodulin and calcium stimulated cyclic nucleotide phosphodiesterase  
 PT - used e.g to identify selective modulators, potentially useful as e.g.  
 PT cardiotonic, antidepressant, antihypertensive agents.  
 XX  
 XX Example 5; Col 85-90; 69pp; English.  
 XX  
 XX The present sequence represents cyclic-GMP-nucleotide phosphodiesterase  
 CC (cgs-PDE), and is isolated from bovine. The specification describes  
 CC calcium ion/calmodulin stimulated cyclic nucleotide phosphodiesterases  
 CC (Cam-PDEs). Cam-PDEs are characterised by their responsiveness to  
 CC intracellular calcium, which leads to a decreased intracellular  
 CC concentration of cAMP and/or cGMP. Cam-PDEs, and their fragments or  
 CC synthetic peptides, are used in therapy, prognosis and diagnosis. They  
 CC are also used to generate specific antibodies useful as immunoassay  
 CC reagents for detecting the protein or for affinity purification and for  
 CC identifying specific modulators of Cam-PDE activity. Cam-PDEs are  
 CC implicated in signalling involving extracellular hormones and  
 CC neurotransmitters, so selective inhibitors are potentially useful as  
 CC cardiotonic, antidepressant, antihypertensive and antithrombotic agents  
 XX  
 XX SQ Sequence 942 AA;

Query Match 100.0%; Score 4911; DB 2; Length 942;  
 Best Local Similarity 100.0%; Pred. No. 0;  
 Matches 942; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 MGQACGHSILCRSQYPAARPAEPGRGQVFLKPDPEPPPPQPCADSLQDALLSLGSLVIDV 60  
 Db 1 MGQACGHSILCRSQYPAARPAEPGRGQVFLKPDPEPPPPQPCADSLQDALLSLGSLVIDV 60

Qy 61 AGLQAVKEALSAVLPKVETVYTYLLDGSRLVCEPPHPELPQEGKREAVISRKLGCN 120  
 Db 61 AGLQAVKEALSAVLPKVETVYTYLLDGSRLVCEPPHPELPQEGKREAVISRKLGCN 120

Qy 121 GLGPSDLPGKPLARLVAFLADPTQVLTPLVDKAGAAVAVILVHCQGLSNEWSLQAV 180  
 Db 121 GLGPSDLPGKPLARLVAFLADPTQVLTPLVDKAGAAVAVILVHCQGLSNEWSLQAV 180

Qy 181 EKHTLVALKRYVALQORESSVAPEATQNPPEEAAGDQKGGVAYTDQDKILQLCGELYDL 240  
 Db 181 EKHTLVALKRYVALQORESSVAPEATQNPPEEAAGDQKGGVAYTDQDKILQLCGELYDL 240

Qy 241 DASSLQLKVLQYLOEQTAQSCCLLLVSEDNLQLSCKVIGDKVLEEBISFPLTTGRLGQV 300  
 Db 241 DASSLQLKVLQYLOEQTAQSCCLLLVSEDNLQLSCKVIGDKVLEEBISFPLTTGRLGQV 300

Qy 301 VEDKKSILQKDLTSEDMLQSLGCEVQAMLCVPVISRATDQVVALACAFNKLGGLFT 360  
 Db 301 VEDKKSILQKDLTSEDMLQSLGCEVQAMLCVPVISRATDQVVALACAFNKLGGLFT 360

Qy 361 DQDEHVIOHCFHYTSTVLSTLAFQEKQKCEQALLQVAKNLFTHLDDVSVLLQREIIT 420  
 Db 361 DQDEHVIOHCFHYTSTVLSTLAFQEKQKCEQALLQVAKNLFTHLDDVSVLLQREIIT 420

Qy 421 EARNLSNAEICSVELLDQNELVAKVFDGGVVEDESYEIRIPADOGIAGHVATTGQILNIP 480  
 Db 421 EARNLSNAEICSVELLDQNELVAKVFDGGVVEDESYEIRIPADOGIAGHVATTGQILNIP 480

Qy 481 DAYAHPFLYRGVDDSTGFRTRNIIICFPFKIKNENQEVIGVAELVNKINGPWFSEKDEDLATA 540  
 Db 481 DAYAHPFLYRGVDDSTGFRTRNIIICFPFKIKNENQEVIGVAELVNKINGPWFSEKDEDLATA 540

Qy 541 FSIYCGISIAHSLLYKKVNEAQYRSHLANEMMMTHMKVSDDEYTKLLHDGQIPVAAIDSN 600  
 Db 541 FSIYCGISIAHSLLYKKVNEAQYRSHLANEMMMTHMKVSDDEYTKLLHDGQIPVAAIDSN 600

Qy 601 FASETYTPRSIPEDDTSMAILSMLODMNFNNYKIDCPTLARFCIMVKKGYPDPYHNMW 660  
 Db 601 FASETYTPRSIPEDDTSMAILSMLODMNFNNYKIDCPTLARFCIMVKKGYPDPYHNMW 660

Qy 661 HAFSVSHFCVLLYKNLEITNYLEDMEIFALFISCMCHDLDRGTNNSFQVASKSVLAALY 720  
 Db 661 HAFSVSHFCVLLYKNLEITNYLEDMEIFALFISCMCHDLDRGTNNSFQVASKSVLAALY 720

Qy 721 SSEGSMVERHHFAQAIAILNTHGNCNIFDHFSPKDYQRMLDLMRDIIILATDLAHHLRIFKD 780  
 Db 721 SSEGSMVERHHFAQAIAILNTHGNCNIFDHFSPKDYQRMLDLMRDIIILATDLAHHLRIFKD 780

Qy 781 LQKMAEYGYDRTNKHSHSLLLCLLMTSCDLSDDQTKGKWTTKIAELIYKEFPFSGDLSEKA 840  
 Db 781 LQKMAEYGYDRTNKHSHSLLLCLLMTSCDLSDDQTKGKWTTKIAELIYKEFPFSGDLSEKA 840

Qy 841 MGNRPMEMDMREKAYIPELQISFMEHIAMPYIKLLQDLFPKAAELYERVAASNREHWTKVS 900  
 Db 841 MGNRPMEMDMREKAYIPELQISFMEHIAMPYIKLLQDLFPKAAELYERVAASNREHWTKVS 900

Qy 901 HKFTIRGLPSNNSLDFFDEEYVDPDLGAPINGCCSLDAE 942  
 Db 901 HKFTIRGLPSNNSLDFFDEEYVDPDLGAPINGCCSLDAE 942

RESULT 7  
 AAY80985  
 ID AAY80985 standard; protein; 942 AA.  
 XX  
 XX AC AAY80985;  
 XX  
 XX DT 05-JUN-2000 (first entry)  
 XX  
 XX DE Bovine brain cgs-PDE, SEQ ID NO:43.  
 XX  
 XX KW Phosphodiesterase; calcium; calmodulin; cyclic guanidine monophosphate;  
 KW cGMP; cyclic nucleotide; messenger; signal transduction; regulation;  
 KW inhibitor; cardiotonic; antidepressant; antihypertensive; antithrombotic.  
 XX  
 XX OS Bos taurus.  
 XX  
 XX PN US6015677-A.  
 XX  
 XX PD 18-JAN-2000.  
 XX  
 XX PF 25-AUG-1998; 98US-00139491.  
 XX  
 XX PR 19-APR-1991; 91US-00688356.  
 XX PR 20-APR-1992; 92US-00872644.  
 XX PR 29-AUG-1994; 94US-00297494.  
 XX PR 31-MAY-1995; 95US-00455525.  
 XX  
 XX PA (UNIW ) UNIV WASHINGTON.  
 XX  
 XX PI Charbonneau H, Sonnenburg WK, Bentley KJ, Beavo JA;  
 XX  
 XX DR WPI; 2000-181142/16.  
 XX DR N-PSDB; AAZ90380.  
 XX  
 XX Assay for inhibitors of cyclic guanidine monophosphate-stimulated  
 PT nucleotide phosphodiesterase, potentially useful as cardiotonic agents.

PT from their ability to alter a heat-shock phenotype.

XX Claim 1; Col 85-90; 69pp; English.

XX The invention relates to purified and isolated nucleotide sequences  
CC encoding mammalian Ca2+/calmodulin-stimulated phosphodiesterases (CaM-  
CC PDEs) and cyclic guanine monophosphate (cGMP)-stimulated  
CC phosphodiesterases (cGS-PDEs). In particular the invention relates to an  
CC assay for identifying chemicals that modify the enzymatic activity of a  
CC mammalian cGS-PDE. The PDEs catalyze the hydrolysis of cyclic  
CC nucleotides to their corresponding 5'-nucleoside monophosphates. In this  
CC way they control the cellular concentration of cyclic nucleotides,  
CC thereby regulating the flow of information from extracellular hormones,  
CC neurotransmitters or other signals that use cyclic nucleotides as  
CC messengers. The PDEs in turn are regulated by transmembrane signals or  
CC second messenger ligands such as Ca2+ or cGMP. Inhibitors of these  
CC enzymes are potentially useful as cardiotonics, antidiuretics,  
CC antihypertensives or antithrombotics. The method of the invention can  
CC identify specific inhibitors of particular isoforms of cGS-PDEs.  
CC Sequences AAY80968, AAY80972, AAY80975, AAY80977, AAY80984, and  
CC AAY80988-Y80990 represent isoforms of CaM-PDEs and cGS-PDEs from bovines  
CC and humans  
XX

SQ Sequence 942 AA;

Query Match 100.0%; Score 4911; DB 3; Length 942;  
Best Local Similarity 100.0%; Pred. No. 0;  
Matches 942; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 MQACGHSILCSQQYPAARPAEPGQQVFLKDEPPPPQPCADSLQDALLSLGSVDV 60  
DB 1 MQACGHSILCSQQYPAARPAEPGQQVFLKDEPPPPQPCADSLQDALLSLGSVDV 60  
QY 61 AGLOQAVKALGAVLPKVTVTYLLDGSRLVCEBPPELPOEGKRVAVISRRLGQN 120  
DB 61 AGLOQAVKALGAVLPKVTVTYLLDGSRLVCEBPPELPOEGKRVAVISRRLGQN 120  
QY 121 GLGPSDLPGKPLARLVAPLAPDTQVLVPLVDKEAGAAVAVILVHCGQLSDNEWSLQAV 180  
DB 121 GLGPSDLPGKPLARLVAPLAPDTQVLVPLVDKEAGAAVAVILVHCGQLSDNEWSLQAV 180  
QY 181 EKHILVALKRVQALQORESSVAPEATQNPPEAAGDQKGGVAYTQDRKILQCGELYDL 240  
DB 181 EKHILVALKRVQALQORESSVAPEATQNPPEAAGDQKGGVAYTQDRKILQCGELYDL 240  
QY 241 DASSLQKVLQVLOQETQASRCLLVSDNLQSKVIGDKVLEETSFPLTTGRIGQV 300  
DB 241 DASSLQKVLQVLOQETQASRCLLVSDNLQSKVIGDKVLEETSFPLTTGRIGQV 300  
QY 301 VEDKKSILQKDLTSEDMLQOQSMGCEVQAMLCVPVISRATDQVVALACAFNKLGGDLFT 360  
DB 301 VEDKKSILQKDLTSEDMLQOQSMGCEVQAMLCVPVISRATDQVVALACAFNKLGGDLFT 360  
QY 361 DQEHVIOHCFHYTSTVLSTLAFQKEQKLCCEQALQVAKNLFTHLDDVSVLQEIIT 420  
DB 361 DQEHVIOHCFHYTSTVLSTLAFQKEQKLCCEQALQVAKNLFTHLDDVSVLQEIIT 420  
QY 421 EARNLSNAEICSVFLLDQNELVAKVDGGVDESEYIRIPADQGIAGHATTGQILNIP 480  
DB 421 EARNLSNAEICSVFLLDQNELVAKVDGGVDESEYIRIPADQGIAGHATTGQILNIP 480  
QY 481 DAYAHLPLFYRGVDDSTGFRTRNLCFPIKNENQEVIGVAELVNKINGPWFSDFLDLATA 540  
DB 481 DAYAHLPLFYRGVDDSTGFRTRNLCFPIKNENQEVIGVAELVNKINGPWFSDFLDLATA 540  
QY 541 FSIYCGISIAHSLLYKKVNEAYQYSHLANEMMYHMKVSDSYTKLLHDGIQPVAAIDSN 600  
DB 541 FSIYCGISIAHSLLYKKVNEAYQYSHLANEMMYHMKVSDSYTKLLHDGIQPVAAIDSN 600  
QY 601 PASFTYTPRSILPEDDTSMAILSMLODMFNNYKIDCPTLARFCLMVKKGYEDPPYHNM 660  
DB 601 PASFTYTPRSILPEDDTSMAILSMLODMFNNYKIDCPTLARFCLMVKKGYEDPPYHNM 660

QY 661 HAFSVSHPCYLLYKXLELTNYLEDMEIPALFISCMCHDLDRGTNNNSFQVASKSVLAALY 720  
DB 661 HAFSVSHPCYLLYKXLELTNYLEDMEIPALFISCMCHDLDRGTNNNSFQVASKSVLAALY 720  
QY 721 SSEGSMVERHHPAQAIATILNTHGCNIFDHFPSKDYORMLDLMDRIIATDLAHLHRIFKD 780  
DB 721 SSEGSMVERHHPAQAIATILNTHGCNIFDHFPSKDYORMLDLMDRIIATDLAHLHRIFKD 780  
QY 781 LQMAEYGVYDRTNKQHSLLCLLMTSCDLSQDTKGWTKTRKIAELIYKEFFSQGDLEKA 840  
DB 781 LQMAEYGVYDRTNKQHSLLCLLMTSCDLSQDTKGWTKTRKIAELIYKEFFSQGDLEKA 840  
QY 841 MGNRPMEWMDREKAYIPELOISFMEHIAPIYKLQDLFPKAAELYERVASNREHWTKVS 900  
DB 841 MGNRPMEWMDREKAYIPELOISFMEHIAPIYKLQDLFPKAAELYERVASNREHWTKVS 900  
QY 901 HKFTIRGLPSSNLSDFLDEYEVPLDGGARAPINGCCSLDAE 942  
DB 901 HKFTIRGLPSSNLSDFLDEYEVPLDGGARAPINGCCSLDAE 942  
RESULT 8  
ABUS8724  
ID ABUS8724 standard; protein; 942 AA.  
XX  
AC ABUS8724;  
XX  
DT 15-APR-2003 (first entry)  
XX  
DE Bovine brain cGS-PDE.  
XX  
KW Cow; Ca2+/calmodulin stimulated phosphodiesterase; enzyme; CaM-PDE;  
KW 59KDa CaM-PDE; 61KDa CaM-PDE; 63KDa CaM-PDE; cGS-PDE;  
KW cyclic-GMP-stimulated phosphodiesterase; cardiotonic agent;  
KW antidiuretic; anti-hypertensive; anti-thrombotic.  
XX  
OS Bos taurus.  
XX  
PN US2002151024-A1.  
XX  
PD 17-OCT-2002.  
XX  
PF 18-JUN-2001; 2001US-00883825.  
XX  
PR 19-APR-1991; 91US-00688356.  
PR 20-APR-1992; 92US-00872644.  
PR 31-MAY-1995; 95US-00455526.  
PR 28-JUL-1998; 98US-00123783.  
XX  
XX (UNIW ) UNIV WASHINGTON.  
XX  
XX Beavo JA, Bentley JK, Charbonneau H, Sonnenburg WK;  
XX  
XX WPI; 2003-198291/19.  
XX  
XX N-PSDB; ABX78857.  
XX  
XX New purified and isolated DNA sequence encoding a mammalian  
XX calcium/calmodulin- or cyclic GMP-stimulated cyclic nucleotide  
XX phosphodiesterase polypeptide, useful for therapeutic, diagnostic and  
XX prognostic applications.  
XX  
XX Example 5; Page 46-49; 71pp; English.  
XX  
XX The invention relates to purified and isolated polynucleotide sequence  
XX encoding a mammalian Ca2+/calmodulin- or cyclic GMP-stimulated cyclic  
XX nucleotide phosphodiesterase polypeptide (CaM-PDE and cGS-PDE). Also  
XX included are a DNA vector comprising the novel DNA sequence, a host cell  
XX transformed with the polynucleotide sequence, a polypeptide product of  
XX the expression in the transformed host cell, an antibody specifically  
XX immunoreactive with the polypeptide and assay methods for identifying a  
XX chemical agent which modifies the enzymatic activity of a mammalian CaM-  
XX PDE or cGS-PDE. Disclosed are the cDNA and protein sequences of bovine  
XX 59KDa CaM-PDE, 61KDa CaM-PDE, 63KDa CaM-PDE, cGS-PDE and human 61KDa CaM-

CC PDE and cGS-PDE. The DNA sequence is useful for producing a polypeptide  
 CC having the enzymatic activity of a mammalian CaM-PDE or cGS-PDE which is  
 CC used in therapeutic, diagnostic and prognostic applications and in the  
 CC preparation of antibodies. Isolated chemical agents which are inhibitors  
 CC of PDEs may have anti-depressant, anti- hypertensive or anti-thrombotic  
 CC activities or may be cardiotoxic agents. The present sequence is a Bovine  
 CC CaM-PDE or cGS-PDE (or fragment) of the invention  
 XX  
 SQ Sequence 942 AA;

Query Match 100.0%; Score 4911; DB 6; Length 942;  
 Best Local Similarity 100.0%; Pred. No. 0;  
 Matches 942; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 MGQACGSHILCRSQYPAARPAERPGQVFLKPDPEPPPPPCADSLQDALLSLGSDIV 60  
 Db 1 MGQACGSHILCRSQYPAARPAERPGQVFLKPDPEPPPPPCADSLQDALLSLGSDIV 60  
 Qy 61 AGLOQAVKEALSAVLPKVTETVYLLDGSRLVCEEPHLPQEGKREAVISRKLGCN 120  
 Db 61 AGLOQAVKEALSAVLPKVTETVYLLDGSRLVCEEPHLPQEGKREAVISRKLGCN 120  
 Qy 121 GLGPSDLPGKELARLAPLAPDTQVLPVLDKAGAVAAVILVHCQGLSDNEBMSLQAV 180  
 Db 121 GLGPSDLPGKELARLAPLAPDTQVLPVLDKAGAVAAVILVHCQGLSDNEBMSLQAV 180  
 Qy 181 EKHTLVALKRVAQLQORSSVAPENTQNPPEAAGDQGGVAYTDDRKILQLCGELYDL 240  
 Db 181 EKHTLVALKRVAQLQORSSVAPENTQNPPEAAGDQGGVAYTDDRKILQLCGELYDL 240  
 Qy 241 DASSLQLKVLQVLOQETQASCCLLVSEDNLQLSCKVIGDKVLEEBISPLTTGRIGQV 300  
 Db 241 DASSLQLKVLQVLOQETQASCCLLVSEDNLQLSCKVIGDKVLEEBISPLTTGRIGQV 300  
 Qy 301 VEDKKSILKDLTSEDMOQLSMLGCEVQAMLCVPVISRATDQVVALACAFNKLGGDLFT 360  
 Db 301 VEDKKSILKDLTSEDMOQLSMLGCEVQAMLCVPVISRATDQVVALACAFNKLGGDLFT 360  
 Qy 361 DQDEHVIQCHFYTSTVLSTLAFQKEQKLKCEQALLQVAKNLFTHLDDVSVLQELIIT 420  
 Db 361 DQDEHVIQCHFYTSTVLSTLAFQKEQKLKCEQALLQVAKNLFTHLDDVSVLQELIIT 420  
 Qy 421 EARLNSNAEICSVFLDQNEILVAKVFDGCVGVEDSEYRIPADQGIAGHVATTQIILNIP 480  
 Db 421 EARLNSNAEICSVFLDQNEILVAKVFDGCVGVEDSEYRIPADQGIAGHVATTQIILNIP 480  
 Qy 481 DAYAHLFYRGVDSSTGFRTRNLCFPPIKNEQVIGVIAELVNKINGPWFSKFDEDLATA 540  
 Db 481 DAYAHLFYRGVDSSTGFRTRNLCFPPIKNEQVIGVIAELVNKINGPWFSKFDEDLATA 540  
 Qy 541 FSIYCGISIAHSLLYKKVNEAQYRSHLANEMMMYHKVSDDEYTKLLHDGIPVAAIDSN 600  
 Db 541 FSIYCGISIAHSLLYKKVNEAQYRSHLANEMMMYHKVSDDEYTKLLHDGIPVAAIDSN 600  
 Qy 601 FASFTYPRSPEDDTSNAIISMLQDMNFINNYKIDCPTLAFCLMWKVGKDYRDPYNNWM 660  
 Db 601 FASFTYPRSPEDDTSNAIISMLQDMNFINNYKIDCPTLAFCLMWKVGKDYRDPYNNWM 660  
 Qy 661 HAFVSVHFYLLYKNLELTYNLEDMEIFALPISCMCHDLDRGTNNSFQVASKSVLAALY 720  
 Db 661 HAFVSVHFYLLYKNLELTYNLEDMEIFALPISCMCHDLDRGTNNSFQVASKSVLAALY 720  
 Qy 721 SSEGSMERHHFAQAIILNTHGNCIFDHFGRKDYQRMMLDMRDIIILATDLAHLRIFKD 780  
 Db 721 SSEGSMERHHFAQAIILNTHGNCIFDHFGRKDYQRMMLDMRDIIILATDLAHLRIFKD 780  
 Qy 781 LQKMAEYGYDRNKHSHLLCLLMTSCDLSQDTKGWTKTKIAELIYKEFFSGDLEKA 840  
 Db 781 LQKMAEYGYDRNKHSHLLCLLMTSCDLSQDTKGWTKTKIAELIYKEFFSGDLEKA 840  
 Qy 841 MGNRPMEMMDREKAYIPELQISFMEHIAAMPYIKLLQDLFPKAAELYERVAASNRHWTKVS 900  
 Db 841 MGNRPMEMMDREKAYIPELQISFMEHIAAMPYIKLLQDLFPKAAELYERVAASNRHWTKVS 900

Qy 301 HKFTIRGLPSNNSLDFLDEEYVDPDLGAPINGCCSLDAE 942  
 Db 301 HKFTIRGLPSNNSLDFLDEEYVDPDLGAPINGCCSLDAE 942

RESULT 9

ADQ94963

ID ADQ94963 standard; protein; 942 AA.

XX AC ADQ94963;

XX DT 23-SEP-2004 (first entry)

XX DE Bovine cGS-PDE protein, pBBCGSPDE-7.

XX DE CaM-PDE;

XX KW Ca 2+/ calmodulin stimulated cyclic nucleotide phosphodiesterase; cGMP;

XX KW cyclic-guanosine monophosphate; cGS-PDE;

XX KW cyclic-GMP stimulated cyclic nucleotide phosphodiesterase; bovine.

XX OS Bos sp.

XX FN US2004126866-A1.

XX PD 01-JUL-2004.

XX PF 30-OCT-2003; 2003US-00697894.

XX PR 19-APR-1991; 91US-00688356.

XX PR 20-APR-1992; 92US-00872644.

XX PR 29-AUG-1994; 94US-00297494.

XX PR 31-MAY-1995; 95US-00455526.

XX PR 28-JUL-1998; 98US-00123783.

XX PR 18-JUN-2001; 2001US-00883825.

XX PA (BEAV/) BEAVO J A.

XX PA (BENT/) BENTLEY J K.

XX PA (CHAR/) CHARBONNEAU H.

XX PA (SONN/) SONNENBURG W K.

XX PI Beavo JA, Bentley JK, Charbonneau H, Sonnenburg WK;

XX DR WPI; 2004-516912/49.

XX DR N-PSDB; ADQ94962.

XX PT Novel mammalian calcium/calmodulin stimulated cyclic phosphodiesterase

XX PT nucleotide sequence useful for identifying chemical agent that modifies

XX PT enzymatic activity of calcium/calmodulin stimulated cyclic

XX PT phosphodiesterase polypeptide.

XX PS Example 5; SEQ ID NO 43; 72pp; English.

XX CC The present invention provides a mammalian Ca 2+/ calmodulin stimulated

XX CC cyclic nucleotide phosphodiesterase (CaM-PDE) and cyclic-guanosine

XX CC monophosphate (cGMP) stimulated cyclic nucleotide phosphodiesterase (cGS-

XX CC PDE) polypeptide and its polynucleotide. The invention is useful for

XX CC producing a polypeptide having enzymatic activity of mammalian CaM-PDE

XX CC and cGS-PDE. The invention is also useful for identifying a chemical

XX CC agent that modifies the enzymatic activity of mammalian CaM-PDE and cGS-

XX CC PDE. The present sequence is bovine cGS-PDE protein, pBBCGSPDE-7.

XX SQ Sequence 942 AA;

Query Match 100.0%; Score 4911; DB 8; Length 942;

Best Local Similarity 100.0%; Pred. No. 0;

Matches 942; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 MGQACGSHILCRSQYPAARPAERPGQVFLKPDPEPPPPPCADSLQDALLSLGSDIV 60

Db 1 MGQACGSHILCRSQYPAARPAERPGQVFLKPDPEPPPPPCADSLQDALLSLGSDIV 60

Qy 61 AGLOQAVKEALSAVLPKVTETVYLLDGSRLVCEEPHLPQEGKREAVISRKLGCN 120



Db 61 AGLOQAVKEALSAVLPKVTETVYLLDGSRLVCEPPHQLPQEGKVRNAVSRKRLGCN 120  
QY 121 GLGPSDLPGKPLARLVAFLAPDQTVLVIPLVDKEAGAAVAVILVHCGQLSDNEEWSLOAV 180  
Db 121 GLGPSDLPGKPLARLVAFLAPDQTVLVIPLVDKEAGAAVAVILVHCGQLSDNEEWSLOAV 180  
QY 181 EKHTLVALKRVQALQORESSVAPEATQNPPEBAAGDQKGGVAYTQDQKILQCGELYDL 240  
Db 181 EKHTLVALKRVQALQORESSVAPEATQNPPEBAAGDQKGGVAYTQDQKILQCGELYDL 240  
QY 241 DASSLQLKVLQYLOQETOASRCLLLVSEDNLQSKVIGDKVLEEEISFPFLLTGRGQV 300  
Db 241 DASSLQLKVLQYLOQETOASRCLLLVSEDNLQSKVIGDKVLEEEISFPFLLTGRGQV 300  
QY 301 VEDKKSILQKDLTSEDMDQQLQSMGCEVQAMLCVPIVSRATQDVVALACAFNKLGGDLFT 360  
Db 301 VEDKKSILQKDLTSEDMDQQLQSMGCEVQAMLCVPIVSRATQDVVALACAFNKLGGDLFT 360  
QY 361 DQDEHVIQCHFYHTSTVLTSTLAFQKEQKLKCECQALLQVAKNLFTHLDDVSVLQEIIT 420  
Db 361 DQDEHVIQCHFYHTSTVLTSTLAFQKEQKLKCECQALLQVAKNLFTHLDDVSVLQEIIT 420  
QY 421 EARNLSNAEICSVFLLDQNELVAKVFDGGVVEDESYEIRIPADQGIAGHVATTGQILNIP 480  
Db 421 EARNLSNAEICSVFLLDQNELVAKVFDGGVVEDESYEIRIPADQGIAGHVATTGQILNIP 480  
QY 481 DAYAHLPLVRGVDDSTGFRNLCPPIKNEQVEIGVAVELVKNKINGPMWFSKFDSDATA 540  
Db 481 DAYAHLPLVRGVDDSTGFRNLCPPIKNEQVEIGVAVELVKNKINGPMWFSKFDSDATA 540  
QY 541 FSIYCGISIAHSLLYKKVNEAQYRSHLANEMMYHMKVSDDEYTKLLHDGIGQFVAADSN 600  
Db 541 FSIYCGISIAHSLLYKKVNEAQYRSHLANEMMYHMKVSDDEYTKLLHDGIGQFVAADSN 600  
QY 601 PASFTYTPRSLPDDTSMALLSMLQDMNFINNYKIDCPTLAFCLMVKGYRDPYHNWM 660  
Db 601 PASFTYTPRSLPDDTSMALLSMLQDMNFINNYKIDCPTLAFCLMVKGYRDPYHNWM 660  
QY 661 HAFSVSHFCYLLKNELTNYLEDMEIPALFTSCMCHDLDRGTNNNSFOVASKSVLAALY 720  
Db 661 HAFSVSHFCYLLKNELTNYLEDMEIPALFTSCMCHDLDRGTNNNSFOVASKSVLAALY 720  
QY 721 SSEGSMERHHPAQAIILNTHGNCIFDHFSRKYQRMFLMRDILATDLAHLRIFKD 780  
Db 721 SSEGSMERHHPAQAIILNTHGNCIFDHFSRKYQRMFLMRDILATDLAHLRIFKD 780  
QY 781 LQKMAEVGYDRTNKQHHSLLLCLLMTSCDLSQDTKGWKTTRKIAELIYKEPFSQGDLEKA 840  
Db 781 LQKMAEVGYDRTNKQHHSLLLCLLMTSCDLSQDTKGWKTTRKIAELIYKEPFSQGDLEKA 840  
QY 841 MGNRPMEWMMDREKAYIPELQISFMHIAMPIYKLLQDLFPKAAELYERVASNRHHTKVS 900  
Db 841 MGNRPMEWMMDREKAYIPELQISFMHIAMPIYKLLQDLFPKAAELYERVASNRHHTKVS 900  
QY 901 HKFTIRGLPSNNSLDFLDEEYVPLDGLARAPINGCCSILDAE 942  
Db 901 HKFTIRGLPSNNSLDFLDEEYVPLDGLARAPINGCCSILDAE 942

RESULT 10  
AAR28408  
ID AAR28408 standard; protein; 942 AA.

XX AAR28408;  
XX AAR28408;  
XX 25-MAR-2003 (revised)  
DT 19-MAR-1993 (first entry)

XX CGS PDE from bovine brain clone pBBCGSPDE-7.  
XX Cyclic GMP; stimulated; cyclic; nucleotide; bovine brain;  
KW phosphodiesterase; hybridisation; ss.

XX OS Bos taurus.  
XX PN W09218541-A1.  
XX PD 29-OCT-1992.  
XX PF 20-APR-1992; 92WO-US003222.  
XX PR 19-APR-1991; 91US-00688356.  
XX PA (UNIW ) UNIV WASHINGTON.  
XX PI Beavo JA, Bentley JK, Charbonneau H, Sonnenburg WK;  
XX DR WPI; 1992-382051/46.  
XX N-PSDB; AAQ30183.  
XX PT New DNA encoding mammalian cyclic nucleotide phospho-di-esterase - and  
XX derived vectors and host cells, useful for screening cpds. for inhibitory  
XX or activating activity.  
XX PS Example 5B; Page 91; 133pp; English.  
XX CC A bovine brain cDNA library in lambda ZAP was screened with a 450 bp  
CC Scori/apai fragment of p3CGS-5 cDNA corresp. to p3CGS-5 nucleotide  
CC position numbers 1-452. Forty putative clones were picked from this first  
CC screen, of which six were randomly selected and purified. Each of the  
CC clones was spotted onto a lawn of host X11 cells and screened with a 370  
CC bp PstI/SmaI fragment of p3CGS-5 cDNA. Six putative clones were obtd. and  
CC sequenced. Clone pBBCGSPDE-7 contains an insert contg. an ORF encoding a  
CC 942 residue protein that is nearly identical to the adrenal gland CGS-PDE  
CC isozyme. The difference in the primary structure of these two isozymes  
CC lies in the amino terminal residues 1-46 of the brain CGS PDE and  
CC residues 1-25 of the adrenal CGS PDE. The remaining carboxy-terminal  
CC residues of the brain and adrenal CGS PDE are identical. (Updated on 25-  
CC MAR-2003 to correct PN field.)  
XX SQ Sequence 942 AA;

Query Match 99.2%; Score 4871; DB 2; Length 942;  
Best Local Similarity 99.2%; Pred. No. 0;  
Matches 934; Conservative 4; Mismatches 4; Indels 0; Gaps 0;

QY 1 MQACGCHILCSQQYPAARPAEPGRGQVFLKPDPPPPPPQPCADSLQDALLSLGSDIV 60  
Db 1 MQACGCHILCSQQYPAARPAEPGRGQVFLKPDPPPPPPQPCADSLQDALLSLGSDIV 60  
QY 61 AGLOQAVKEALSAVLPKVTETVYLLDGSRLVCEPPHQLPQEGKVRNAVSRKRLGCN 120  
Db 61 AGLOQAVKEALSAVLPKVTETVYLLDGSRLVCEPPHQLPQEGKVRNAVSRKRLGCN 120  
QY 121 GLGPSDLPGKPLARLVAFLAPDQTVLVIPLVDKEAGAAVAVILVHCGQLSDNEEWSLOAV 180  
Db 121 GLGPSDLPGKPLARLVAFLAPDQTVLVIPLVDKEAGAAVAVILVHCGQLSDNEEWSLOAV 180  
QY 181 EKHTLVALKRVQALQORESSVAPEATQNPPEBAAGDQKGGVAYTQDQKILQCGELYDL 240  
Db 181 EKHTLVALKRVQALQORESSVAPEATQNPPEBAAGDQKGGVAYTQDQKILQCGELYDL 240  
QY 241 DASSLQLKVLQYLOQETOASRCLLLVSEDNLQSKVIGDKVLEEEISFPFLLTGRGQV 300  
Db 241 DASSLQLKVLQYLOQETOASRCLLLVSEDNLQSKVIGDKVLEEEISFPFLLTGRGQV 300  
QY 301 VEDKKSILQKDLTSEDMDQQLQSMGCEVQAMLCVPIVSRATQDVVALACAFNKLGGDLFT 360  
Db 301 VEDKKSILQKDLTSEDMDQQLQSMGCEVQAMLCVPIVSRATQDVVALACAFNKLGGDLFT 360  
QY 361 DQDEHVIQCHFYHTSTVLTSTLAFQKEQKLKCECQALLQVAKNLFTHLDDVSVLQEIIT 420  
Db 361 DQDEHVIQCHFYHTSTVLTSTLAFQKEQKLKCECQALLQVAKNLFTHLDDVSVLQEIIT 420  
QY 421 EARNLSNAEICSVFLLDQNELVAKVFDGGVVEDESYEIRIPADQGIAGHVATTGQILNIP 480

|||||  
421 EARNLSNAEISCVFLDQNELVAKVDFGVLEDESVEIRIPADQGIAGHVATTGQILNIP 480  
QY 481 DAYAHPFYRGVDDSTGFRTRNLCFPPIKNEQVIGVAELVKNKINGPWFSKFDEDLATA 540  
Db 481 DAYAHPFYRGVDDSTGFRTRNLCFPPIKNEQVIGVAELVKNKINGPWFSKFDEDLATA 540  
QY 541 FSIYCGISIAHSLLYKKVNEAQYRSHLANEMMMYHMKVSDDEYTKLLHDGIGPVAADISN 600  
Db 541 FSIYCGISIAHSLLYKKVNEAQYRSHLANEMMMYHMKVSDDEYTKLLHDGIGPVAADISN 600  
QY 601 FASFTYTPRSLPEDDTSMAILSMLQDMNFNNYKIDCPTLARFCLMVKKGYRDPYHNWM 660  
Db 601 FASFTYTPRSLPEDDTSMAILSMLQDMNFNNYKIDCPTLARFCLMVKKGYRDPYHNWM 660  
QY 661 HAFSVSHFCYLLYKNLELTNYLEDMEIFALFISCMCHDLHRGTNNNSFQVASKSVLAALY 720  
Db 661 HAFSVSHFCYLLYKNLELTNYLEDMEIFALFISCMCHDLHRGTNNNSFQVASKSVLAALY 720  
QY 721 SSEGSVMERHHFAQAIATLNTHGNCNIFDHFSRKDYQRMQLDMRDIILATDLAHLRIPKD 780  
Db 721 SSEGSVMERHHFAQAIATLNTHGNCNIFDHFSRKDYQRMQLDMRDIILATDLAHLRIPKD 780  
QY 781 LQKMAEVGYDRTNKQHSLLCLLMTSCDLSQDTKGWKTTRKIAELIYKFFSQGDLEKA 840  
Db 781 LQKMAEVGYDRTNKQHSLLCLLMTSCDLSQDTKGWKTTRKIAELIYKFFSQGDLEKA 840  
QY 841 MGNRPMEHMDREKAYIPELOISFMEHIAPIYKLLQDLFPKAAELYERVAASNRHWTKVS 900  
Db 841 MGNRPMEHMDREKAYIPELOISFMEHIAPIYKLLQDLFPKAAELYERVAASNRHWTKVS 900  
QY 901 HKFTIRGLPSNNSLDYDEEYEVPLDGCARAPINGCCSLDAE 942  
Db 901 HKFTIRGLPSNNSLDYDEEYEVPLDGCARAPINGCCSLDAE 942

## RESULT 11

AAR69729  
ID AAR69729 standard; protein; 941 AA.  
XX  
AC AAR69729;  
XX  
DT 25-MAR-2003 (revised)  
DT 11-OCT-1995 (first entry)  
XX  
XX Cyclic-GMP stimulated nucleotide PDE clone HFB9.2.  
DE  
XX Cyclic-GMP stimulated nucleotide phosphodiesterase; antibodies; human;  
KW hormones; neurotransmitters; transmission regulation;  
KW enzyme purification; clone HFB9.2.  
XX  
OS Homo sapiens.  
XX  
FN US5389527-A.  
XX  
PD 14-FEB-1995.  
XX  
FF 20-APR-1992; 92US-00872644.  
XX  
PR 19-APR-1991; 91US-00688356.  
XX  
PA (UNIW ) UNIV WASHINGTON.  
XX  
FI Sonnenburg WK, Charbonneau H, Beavo JA;  
XX  
DR WPI; 1995-090205/12.  
DR N-PSDB; AAQ83978.  
XX  
PT New nucleic acid encoding cyclic-GMP stimulated nucleotide phospho-  
diesterase - and related vectors and transformed cells, useful for  
PT screening cpds. for phospho-diesterase modulating activity.  
XX  
PS Claim 1; Col 89-96; 69pp; English.

XX AAQ83978 encodes AAR69729 the human cyclic-GMP stimulated nucleotide  
CC phosphodiesterase (Cam PDE) clone HFB9.2. Eukaryotic cells that express  
CC Cam PDE can be used to screen cpds. for the ability to modulate Cam PDE  
CC activity. Cam PDEs are involved in regulating the transmission of  
CC information from hormones, neurotransmitters or other systems that use  
CC cyclic nucleotides as messengers. Antibodies raised against Cam PDE can  
CC be used for enzyme purification, or determination. (Updated on 25-MAR-2003 to  
CC correct PF field.)  
XX  
SQ Sequence 941 AA;

Query Match 96.3%; Score 4728.5; DB 2; Length 941;  
Best Local Similarity 96.0%; Pred. No. 0;  
Matches 904; Conservative 18; Mismatches 19; Indels 1; Gaps 1;  
QY 1 MGQACGHSILCRSQOYPAARPAEPGRGOVFLKPDPPPPPPPCADSLQDALLSLGSDIVD 60  
Db 1 MGQACGHSILCRSQOYPAARPAEPGRGOVFLKPDPPPPPPPCADSLQDALLSLGSDIVI 60  
QY 61 AGLOQAVKEALSAVLPKVTYTYLLDGESPLVCEEPHELPOEGKVEAVISRKLGCN 120  
Db 61 SGLQRAVKEALSAVLPKVTYTYLLDGESPLVCEEPHELPOEGKVEAVISRKLGCN 120  
QY 121 GLGSDLPGRPLARLAPLAPDTQVLPVLDKAGAAVAVILVHCGQLSNEEWSLOAV 180  
Db 121 GLGSDLPGRPLARLAPLAPDTQVLPVLDKAGAAVAVILVHCGQLSNEEWSLOAV 180  
QY 181 EKHTLVALKRVQALQORESSVAPATQNPPEAAGDQGGVAYTDQDRKILQLCGELYDL 240  
Db 181 EKHTLVALKRVQALQORESSVAPATQNPPEAAGDQGGVAYTDQDRKILQLCGELYDL 240  
QY 241 DASSLQILKVLYLOQETQASRCLLYSEDNLQISCKVIGDKVLEESFPILTGRIGOV 300  
Db 241 DASSLQILKVLYLOQETQASRCLLYSEDNLQISCKVIGDKVLEESFPILTGRIGOV 300  
QY 301 VEDKKSILQKDLTSEDMMQQLSMLGCEVQAMLCPVVISRATDQVVVALACAFNKLGGDLFT 360  
Db 301 VEDKKSILQKDLTSEDMMQQLSMLGCEVQAMLCPVVISRATDQVVVALACAFNKLGGDLFT 360  
QY 361 DQDEHVIQHCFTYTSVLTSTLAFQKQKCECOALLQVAKNLFTHLDDVSVLQEIIT 420  
Db 361 DQDEHVIQHCFTYTSVLTSTLAFQKQKCECOALLQVAKNLFTHLDDVSVLQEIIT 420  
QY 421 EARNLSNAEISCVFLLDQNELVAKVDFGVLEDESVEIRIPADQGIAGHVATTGQILNIP 480  
Db 421 EARNLSNAEISCVFLLDQNELVAKVDFGVLEDESVEIRIPADQGIAGHVATTGQILNIP 480  
QY 481 DAYAHPFYRGVDDSTGFRTRNLCFPPIKNEQVIGVAELVKNKINGPWFSKFDEDLATA 540  
Db 481 DAYAHPFYRGVDDSTGFRTRNLCFPPIKNEQVIGVAELVKNKINGPWFSKFDEDLATA 540  
QY 541 FSIYCGISIAHSLLYKKVNEAQYRSHLANEMMMYHMKVSDDEYTKLLHDGIGPVAADISN 600  
Db 541 FSIYCGISIAHSLLYKKVNEAQYRSHLANEMMMYHMKVSDDEYTKLLHDGIGPVAADISN 600  
QY 601 FASFTYTPRSLPEDDTSMAILSMLQDMNFNNYKIDCPTLARFCLMVKKGYRDPYHNWM 660  
Db 601 FASFTYTPRSLPEDDTSMAILSMLQDMNFNNYKIDCPTLARFCLMVKKGYRDPYHNWM 660  
QY 661 HAFSVSHFCYLLYKNLELTNYLEDMEIFALFISCMCHDLHRGTNNNSFQVASKSVLAALY 720  
Db 661 HAFSVSHFCYLLYKNLELTNYLEDMEIFALFISCMCHDLHRGTNNNSFQVASKSVLAALY 720  
QY 721 SSEGSVMERHHFAQAIATLNTHGNCNIFDHFSRKDYQRMQLDMRDIILATDLAHLRIPKD 780  
Db 721 SSEGSVMERHHFAQAIATLNTHGNCNIFDHFSRKDYQRMQLDMRDIILATDLAHLRIPKD 780  
QY 781 LQKMAEVGYDRTNKQHSLLCLLMTSCDLSQDTKGWKTTRKIAELIYKFFSQGDLEKA 840  
Db 781 LQKMAEVGYDRTNKQHSLLCLLMTSCDLSQDTKGWKTTRKIAELIYKFFSQGDLEKA 840  
QY 841 MGNRPMEHMDREKAYIPELOISFMEHIAPIYKLLQDLFPKAAELYERVAASNRHWTKVS 900  
Db 841 MGNRPMEHMDREKAYIPELOISFMEHIAPIYKLLQDLFPKAAELYERVAASNRHWTKVS 900



XX Cyclic-GMP-stimulated phosphodiesterase; antibody; human;  
KW polymerase chain reaction.  
XX Homo sapiens.  
OS US5602019-A.  
PN 11-FEB-1997.  
PD 29-AUG-1994; 94US-00297510.  
PF 19-APR-1991; 91US-00688356.  
PR 20-APR-1992; 92US-00872644.  
XX (UNIW ) UNIV WASHINGTON.  
XX Sonnenburg WK, Charbonneau H, Bentley JK, Beavo JA;  
PI WPI; 1997-131799/12.  
DR N-ESDB; AAT67224.  
XX DNA encoding bovine and human phosphodiesterase enzymes - stimulated by  
PT calcium/calmodulin, useful for recombinant prodn. of the enzymes.  
XX Example 6; Col 97-102; 69pp; English.  
XX The present sequence represents the human cyclic-GMP-stimulated  
CC phosphodiesterase (cGS-PDE) from pHCs6n plasmid. The DNA sequences of  
CC the cGS-PDE's are used for the production of the recombinant enzymes,  
CC which in turn may be used for antibody production and to screen for  
CC compounds that modulate phosphodiesterase activity. (Updated on 25-MAR-  
CC 2003 to correct PF field.) (Updated on 25-MAR-2003 to correct PI field.)  
XX SQ Sequence 941 AA;  
Query Match 96.3%; Score 4728.5; DB 2; Length 941;  
Best Local Similarity 96.0%; Pred. No. 0;  
Matches 904; Conservative 18; Mismatches 19; Indels 1; Gaps 1;  
QY 1 MGQACGHSILCRSQQYPAARPAEPGRQGVFLKPDPEPPPPQPCADSLQDALLSLGSDVD 60  
DB 1 MGQACGHSILCRSQQYPAARPAEPGRQGVFLKPDPEPPPPQPCADSLQDALLSLGSDVDI 60  
QY 61 AGLQAVKEALSAVLPRVETVYTYLLDGSRLVCEPPEPHELPOEGKVREAVISRKLGCN 120  
DB 61 SGLQRAVKEALSAVLPRVETVYTYLLDGSRLVCEPPEPHELPOEGKVREAVISRKLGCN 120  
QY 121 GLGFSDLPGKPLARLVAFLAPDQVLPVLDKAGAAVAVLVHCGQLSDNEEWSLQAV 180  
DB 121 GLGFSDLPGKPLARLVAFLAPDQVLPVLDKAGAAVAVLVHCGQLSDNEEWSLQAV 180  
QY 181 EKHTLVALKRVQALQORESSVAPEATQNPPEAAGDQKGVAYTDQDRKILQLCGELYDL 240  
DB 181 EKHTLVALKRVQALQORESSVAPEATQNPPEAAGDQKGVAYTDQDRKILQLCGELYDL 240  
QY 241 DASSLQLKVLQYLOQETOQASRCLLLVSEDNLQLSCKVIGDKVLEEBISFPLTGRIGQV 300  
DB 241 DASSLQLKVLQYLOQETOQASRCLLLVSEDNLQLSCKVIGDKVLEEBISFPLTGRIGQV 299  
QY 301 VEDKKSICQLKDLTSEDQQLQSMGLGCEVQAMLCVPIVSRATDQVVALACAFNKLGGDLFT 360  
DB 300 VEDKKSICQLKDLTSEDQQLQSMGLGCEVQAMLCVPIVSRATDQVVALACAFNKLGGDLFT 359  
QY 361 DQDEHVIQCHFYTSTVLSTLAFQEKJLKECEQALLQVAKNLFTHLDDVSVLLQEIT 420  
DB 360 DQDEHVIQCHFYTSTVLSTLAFQEKJLKECEQALLQVAKNLFTHLDDVSVLLQEIT 419  
QY 421 EARNLSNAEISCVFLLDQNELVAKVFDGCVVEDESYEIRIPADQGIAGHVATTGQILNIP 480  
DB 420 EARNLSNAEISCVFLLDQNELVAKVFDGCVVEDESYEIRIPADQGIAGHVATTGQILNIP 479  
QY 481 DAYAHPFLYRGVDDSTGFRTRNLCFPIKNEQVIGVAELVNKINGPWFPSKFDLATA 540

DB 480 DAYAHPFLYRGVDDSTGFRTRNLCFPIKNEQVIGVAELVNKINGPWFPSKFDLATA 539  
QY 541 PSYCGISIAHSLLYKKVNEAQYRSHLANEMMMTHMKVSDDEYTKLLHDGQIPVAAIDSN 600  
DB 540 PSYCGISIAHSLLYKKVNEAQYRSHLANEMMMTHMKVSDDEYTKLLHDGQIPVAAIDSN 599  
QY 601 PASFTYTPRSILPEDDTSMAILSMLQDMNFNNYKIDCPTLARFCIMVKKGVRDPYPHNW 660  
DB 600 PASFTYTPRSILPEDDTSMAILSMLQDMNFNNYKIDCPTLARFCIMVKKGVRDPYPHNW 659  
QY 661 HAFSVSHFCYLLYKNLELTNYLEDMEIFALFISCMCHDLDRGTNNNSQVASKSVLAALY 720  
DB 660 HAFSVSHFCYLLYKNLELTNYLEDIEIFALFISCMCHDLDRGTNNNSQVASKSVLAALY 719  
QY 721 SSEGSMERHHAQAIAILNTHGNCIFDHFPSRKDYQRMQLDMRDILATDLAHLIRIFKD 780  
DB 720 SSEGSMERHHAQAIAILNTHGNCIFDHFPSRKDYQRMQLDMRDILATDLAHLIRIFKD 779  
QY 781 LQKMAEYGYDRTNKHSHLLCLLMTSCDLSDOTKGWKTTRKIAELIYKEFPQSGDLEKA 840  
DB 780 LQKMAEYGYDRTNKHSHLLCLLMTSCDLSDOTKGWKTTRKIAELIYKEFPQSGDLEKA 839  
QY 841 MGNRPMEWMDEKAYIPELQISFMEHIAPIYKLLQDLFPAKAEIYERVAENREHWTKVS 900  
DB 840 MGNRPMEWMDEKAYIPELQISFMEHIAPIYKLLQDLFPAKAEIYERVAENREHWTKVS 899  
QY 901 HKFTIRGLPSNNSLDLDEEYVDPDLCARAPINGCCSLDAE 942  
DB 900 HKFTIRGLPSNNSLDLDEEYVDPDLCARAPINGCCSLDAE 941  
RESULT 14  
AAW71226  
ID AAW71226 standard; protein; 941 AA.  
XX AC AAW71226;  
XX DT 29-OCT-1998 (first entry)  
XX DE Human cGS-PDE cDNA protein sequence.  
XX KW Ca2+/calmodulin sensitive cyclic nucleotide phosphodiesterase; Cam-PDE;  
KW assay; identification; modification; enzymatic activity; modulator;  
KW cyclic guanosine monophosphate-stimulated phosphodiesterase; cGS-PDE;  
XX human.  
XX OS Homo sapiens.  
XX PN US5800987-A.  
XX PD 01-SEP-1998.  
XX PF 31-MAY-1995; 95US-00455525.  
XX PR 19-APR-1991; 91US-00688356.  
XX PR 20-APR-1992; 92US-00872644.  
XX PR 29-AUG-1994; 94US-00297494.  
XX PA (UNIW ) UNIV WASHINGTON.  
XX PI Sonnenburg WK, Charbonneau H, Beavo JA, Bentley JK;  
XX DR WPI; 1998-494762/42.  
XX DR N-ESDB; AAV54762.  
XX PT Identification of modulators of Calcium/calmodulin sensitive cyclic  
PT nucleotide phosphodiesterase - uses recombinant cells expressing the  
PT enzyme and monitoring protein expression in the presence of potential  
XX modulators.  
XX Example 6; Col 97-102; 69pp; English.

CC The present sequence represents human cyclic guanosine monophosphate-  
CC stimulated phosphodiesterase (cG5-PDE) cDNA. The specification also  
CC describes Ca2+/calmodulin sensitive cyclic nucleotide phosphodiesterase  
CC (Cam-PDE) enzymes. Cam-PDE enzymes catalyze the hydrolysis of cyclic  
CC nucleotides and as such control their intracellular level. They are  
CC controlled by second messengers e.g. Ca2+ and calmodulin and  
CC transmembrane signals and through pathways involving these, regulate flow  
CC of information from extracellular hormones, neurotransmitters and other  
CC signals using cyclic nucleotides as messengers. The specification  
CC describes an assay for identifying a chemical agent which modifies the  
CC enzymatic activity of a mammalian Cam-PDE. The assays are useful for  
CC identifying modulators of Cam-PDEs. The assay is carried out by  
CC incubating cells expressing Cam-PDE with the suspected modulator and  
CC measuring its effect e.g. monitoring the hydrolysis of cAMP and/or cGMP  
XX

SQ Sequence 941 AA;

Query Match 96.3%; Score 4728.5; DB 2; Length 941;

Best Local Similarity 96.0%; Pred. No. 0;

Matches 904; Conservative 18; Mismatches 19; Indels 1; Gaps 1;

Qy 1 MQQACGHSILCRSQYPAARPAERPGQVFLKPEDEPPPPQPCADSLQDALLSLGSVIDV 60  
Db 1 MQQACGHSILCRSQYPAARPAERPGQVFLKPEDEPPPPQPCADSLQDALLSLGSVIDI 60  
Qy 61 AGLOQAVKEALSAVLPKVETVYTYLLDGSRLVCBEPPELHPQEGKVRKAVISRKLGCN 120  
Db 61 SGLQRAVKEALSAVLPKVETVYTYLLDGSRLVCBEPPELHPQEGKVRKAVISRKLGCN 120  
Qy 121 GLGPSDLPGKPLARLVAIPAPDTQVLPVLDKKEAGAAVAVILVHCGQLSDNEEWSLOAV 180  
Db 121 GLGPSDLPGKPLARLVAIPAPDTQVLPVLDKKEAGAAVAVILVHCGQLSDNEEWSLOAV 180  
Qy 181 EKHTLVALKRVQALQORESSVAPEATONPPEAAGDKGGVAYTDQDRKILQCGELYDL 240  
Db 181 EKHTLVALKRVQALQORESSVAPEATONPPEAAGDKGGVAYTDQDRKILQCGELYDL 240  
Qy 241 DASSLQLKVLQYLOQETQASRCLLVSDNQLSKCKVIGDKVLEEEISFPITTRGLGV 300  
Db 241 DASSLQLKVLQYLOQETQASRCLLVSDNQLSKCKVIGDKVLEEEISFPITTRGLGV 300  
Qy 301 VEDKKSILQKLTSDMQQLQSMGCEVQAMLCVPVISRATDQVVALACAFNKGDLFT 360  
Db 301 VEDKKSILQKLTSDMQQLQSMGCEVQAMLCVPVISRATDQVVALACAFNKGDLFT 360  
Qy 361 DQDEHVIQCHFYTSTVLTSTLAFQKQKLCCEQALLQVAKNLFTHLDDSVLLQEIIT 420  
Db 361 DQDEHVIQCHFYTSTVLTSTLAFQKQKLCCEQALLQVAKNLFTHLDDSVLLQEIIT 420  
Qy 421 EARLNSNAEICSVFLLDQNELVAKVFDGGVDESEYRIPADQGIAGHVATTGQILNIP 480  
Db 421 EARLNSNAEICSVFLLDQNELVAKVFDGGVDESEYRIPADQGIAGHVATTGQILNIP 480  
Qy 481 DAYAHLFVRGVDSTGFRTRNLCPFKENQEVIGVAELVNKINGPMWFKFDBDLATA 540  
Db 481 DAYAHLFVRGVDSTGFRTRNLCPFKENQEVIGVAELVNKINGPMWFKFDBDLATA 540  
Qy 541 FSIYCGISIAHSLLYKKNEAQYRSHLANEMMYHMKVSDDEYTKLHDGTPVAADSN 600  
Db 541 FSIYCGISIAHSLLYKKNEAQYRSHLANEMMYHMKVSDDEYTKLHDGTPVAADSN 600  
Qy 601 FASFTYTPRSIPEDDTSMAILSMLQDMFNINNYKIDCPTLARFCLMWKGYRDPYHNM 660  
Db 601 FASFTYTPRSIPEDDTSMAILSMLQDMFNINNYKIDCPTLARFCLMWKGYRDPYHNM 660  
Qy 661 HAFVSVHCYLLYKNLELTNYLEDMEIFALFISCMCHDLHRGTNNSQVASKSVLAALY 720  
Db 661 HAFVSVHCYLLYKNLELTNYLEDMEIFALFISCMCHDLHRGTNNSQVASKSVLAALY 720  
Qy 721 SSEGVSWEHHPHQAIAIALNTHGCMIFDHFSRKDYQRMQLDMLRDILATDLAHLRIFKD 780  
Db 721 SSEGVSWEHHPHQAIAIALNTHGCMIFDHFSRKDYQRMQLDMLRDILATDLAHLRIFKD 780  
Qy 779 SSEGVSWEHHPHQAIAIALNTHGCMIFDHFSRKDYQRMQLDMLRDILATDLAHLRIFKD 779  
Db 779 SSEGVSWEHHPHQAIAIALNTHGCMIFDHFSRKDYQRMQLDMLRDILATDLAHLRIFKD 779

Qy 781 LQKMAEVGYDRTNKKQHHSLLCLLMTSCDLSQTKGWKTKRIAEILYKEPFSQGDLEKA 840  
Db 781 LQKMAEVGYDRTNKKQHHSLLCLLMTSCDLSQTKGWKTKRIAEILYKEPFSQGDLEKA 840  
Qy 841 MGNRPMEWMMDREKAYIPELQISFMESHIAPIYKLQDLFPKAAELYERVASNRHWTKVS 900  
Db 841 MGNRPMEWMMDREKAYIPELQISFMESHIAPIYKLQDLFPKAAELYERVASNRHWTKVS 900  
Qy 901 HKFTIRGLPSNNSLDFLDEEYVDPDGLGARAPINGCCSLDAE 942  
Db 901 HKFTIRGLPSNNSLDFLDEEYVDPDGLGARAPINGCCSLDAE 941

RESULT 15

AAW77042

ID AAW77042 standard; protein; 941 AA.

XX AC AAW77042;

XX DT 14-DEC-1998 (first entry)

XX DE Cyclic-GMP-stimulated phosphodiesterase clone pHcgs6n.

XX KW cow; Ca2+ stimulated phosphodiesterase;

XX KW Calmodulin stimulated phosphodiesterase; therapeutic; antibody.

XX OS Bos sp.

XX PN US5789553-A.

XX PD 04-AUG-1998.

XX PF 31-MAY-1995; 95US-00455526.

XX PR 19-APR-1991; 91US-00688356.

XX PR 20-APR-1992; 92US-00872644.

XX PR 29-AUG-1994; 94US-00297494.

XX PA (UNIW ) UNIV WASHINGTON.

XX PI Sonnenburg WK, Charbonneau H, Beavo JA, Bentley JK;

XX DR WPI; 1998-446185/38.

XX DR N-PSDB; AAV48205.

XX PT Antibody to phosphodiesterase polypeptide - useful for purification or

XX PT detection of polypeptide.

XX PS Example 6; Column 89/96; 68pp; English.

XX CC The cyclic-GMP-stimulated phosphodiesterase clone pHcgs6n encodes a  
XX CC phosphodiesterase from the bovine brain. The phosphodiesterases isolated  
XX CC in this invention were used to transform host cells, preferably mammalian  
XX CC or yeast cells. The recombinant proteins and fragments produced can be  
XX CC used for therapeutic, diagnostic, and prognostic purposes and will  
XX CC provide the basis for preparation of monoclonal and polyclonal  
XX CC antibodies. An antibody specific for the Ca2+/calmodulin-stimulated  
XX CC cyclic nucleotide phosphodiesterase (PDE) polypeptide is useful for  
XX CC affinity purification or detection of the polypeptide and is selective  
XX CC only for the Ca2+/calmodulin stimulated cyclic nucleotide PDE polypeptide

XX SQ Sequence 941 AA;

Query Match 96.3%; Score 4728.5; DB 2; Length 941;

Best Local Similarity 96.0%; Pred. No. 0;

Matches 904; Conservative 18; Mismatches 19; Indels 1; Gaps 1;

Qy 1 MQQACGHSILCRSQYPAARPAERPGQVFLKPEDEPPPPQPCADSLQDALLSLGSVIDV 60  
Db 1 MQQACGHSILCRSQYPAARPAERPGQVFLKPEDEPPPPQPCADSLQDALLSLGSVIDI 60  
Qy 61 AGLOQAVKEALSAVLPKVETVYTYLLDGSRLVCBEPPELHPQEGKVRKAVISRKLGCN 120  
Db 61 SGLQRAVKEALSAVLPKVETVYTYLLDGSRLVCBEPPELHPQEGKVRKAVISRKLGCN 120

Db 61 SGLQRAVKEALSAVLPRVETVYTYLLDGSOLVCBPPHELPOEGKVREAIISQKRLGCN 120  
Qy 121 GLGPSDLPGKPLARLAVAPLADPTQVLVPLVDKEAGAAVTLVHCGQISDNEEWSLOAV 180  
Db 121 GLGPSDLPGKPLARLAVAPLADPTQVLVPLVDKEAGAAVTLVHCGQISDNEEWSLOAV 180  
Qy 181 EKHTLVALKRVQALQORRESSVAPEATQNPPEAAAGDQKGGVAYTDQDRKILQLCGELYDL 240  
Db 181 EKHTLVALKRVQALQORRESSVAPEATQNPPEAAAGDQKGGVAYTDQDRKILQLCGELYDL 240  
Qy 241 DASSLQLKVLQYLQOQETQASRCLLVSEDNLQLSCKVIGDKVLEEEISFPLTTGRLGOV 300  
Db 241 DASSLQLKVLQYLQOQETQASRCLLVSEDNLQLSCKVIGDKVLEEEISFPLTTGRLGOV 300  
Qy 301 VEDKKSIOQLKDLTSEDMOQLQSMGLCEVOAMLCVPVISRATDOVVALACAFNKLGGDLFT 360  
Db 300 VEDKKSIOQLKDLTSEDMOQLQSMGLCEVOAMLCVPVISRATDOVVALACAFNKLGGDLFT 360  
Qy 361 DODEHVIQCHFYHTSTVLTSITLAFQKEQKLKCECOALLQVAKNLFTHLDDVSVLLOEIIIT 420  
Db 360 DODEHVIQCHFYHTSTVLTSITLAFQKEQKLKCECOALLQVAKNLFTHLDDVSVLLOEIIIT 420  
Qy 421 EARNLSNAEICSVFLLDQNELVAKVFDGGVVEDESEYIRIPADQGIAGHVATTGQILNIP 480  
Db 420 EARNLSNAEICSVFLLDQNELVAKVFDGGVVEDESEYIRIPADQGIAGHVATTGQILNIP 480  
Qy 481 DAYAHLPLFYRGVDDSTGTRFRNLCFPIKNENQEVIGVLAELVNKINGPWFKFDDEDLATA 540  
Db 480 DAYAHLPLFYRGVDDSTGTRFRNLCFPIKNENQEVIGVLAELVNKINGPWFKFDDEDLATA 540  
Qy 541 FSIYCGISIAHSLLYKKNLQYRSHLANEMMMYHMKVSDDBEYTKLLHDGIQPVAAIDSN 600  
Db 540 FSIYCGISIAHSLLYKKNLQYRSHLANEMMMYHMKVSDDBEYTKLLHDGIQPVAAIDSN 600  
Qy 601 FASFTYTPRSLPEDDTSMAILSMLQDMNFINNYKIDCPTLARFCLMWKKGYRDPYPYHNM 660  
Db 600 FASFTYTPRSLPEDDTSMAILSMLQDMNFINNYKIDCPTLARFCLMWKKGYRDPYPYHNM 660  
Qy 661 HAFVSVSHFCYLLYKNLELTNYLEDMEIFALFISCMCHDLDRGTNNSPQVASKSVLAALY 720  
Db 660 HAFVSVSHFCYLLYKNLELTNYLEDMEIFALFISCMCHDLDRGTNNSPQVASKSVLAALY 720  
Qy 721 SSEGSVMERHHPAQAIALINTHGCNIPDHFSRKYORMLDLMDRIILATDLAHLRIFKD 780  
Db 720 SSEGSVMERHHPAQAIALINTHGCNIPDHFSRKYORMLDLMDRIILATDLAHLRIFKD 780  
Qy 781 LQKMAEVGYDRNKHSHLLCLLMTSCDLSQTKGWKTTRKIAELIYKEFFSQGDLEKA 840  
Db 780 LQKMAEVGYDRNKHSHLLCLLMTSCDLSQTKGWKTTRKIAELIYKEFFSQGDLEKA 840  
Qy 841 MGNRPMENMDREKAYIPLOISFMEHIAMPIYKLLQDLFPKAAELYERVASNREHWTKVS 900  
Db 840 MGNRPMENMDREKAYIPLOISFMEHIAMPIYKLLQDLFPKAAELYERVASNREHWTKVS 900  
Qy 901 HKFTIRGLPSNNSLDLDEEYEVDPDLCGARAPINGCCSLDAB 942  
Db 900 HKFTIRGLPSNNSLDLDEEYEVDPDLCGARAPINGCCSLDAB 941

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OM protein - protein search, using sw model

Run on: June 26, 2005, 12:10:37 ; Search time 30.8438 Seconds  
(without alignments)  
2279.856 Million cell updates/sec

Title: US-10-697-894-43  
Perfect score: 4911  
Sequence: 1 MGQACGHSILCRSQYPAAR.....VPLDGLARAPINGCCSLDAE 942

Scoring table: BLOSUM62  
Gapop 10.0 , Gapext 0.5

Searched: 513545 seqs, 74649064 residues

Total number of hits satisfying chosen parameters: 513545

Minimum DB seq length: 0  
Maximum DB seq length: 2000000000  
Post-processing: Minimum Match 0%  
Maximum Match 100%  
Listing first 45 summaries

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2: /cgn2\_6/ptodata/1/1aa/5B-COMB.pep:\*  
3: /cgn2\_6/ptodata/1/1aa/6A-COMB.pep:\*  
4: /cgn2\_6/ptodata/1/1aa/6B-COMB.pep:\*  
5: /cgn2\_6/ptodata/1/1aa/PCTUS-COMB.pep:\*  
6: /cgn2\_6/ptodata/1/1aa/backfiles1.pep:\*

Pred. No. is the number of results predicted by chance to have a  
score greater than or equal to the score of the result being printed,  
and is derived by analysis of the total score distribution.

## SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	4911	100.0	942	1 US-07-872-644-43	Sequence 43, Appl
2	4911	100.0	942	1 US-08-297-494-43	Sequence 43, Appl
3	4911	100.0	942	1 US-08-297-510-43	Sequence 43, Appl
4	4911	100.0	942	1 US-08-479-532-43	Sequence 43, Appl
5	4911	100.0	942	1 US-08-455-525-43	Sequence 43, Appl
6	4911	100.0	942	1 US-08-455-525-43	Sequence 43, Appl
7	4911	100.0	942	3 US-09-139-491-43	Sequence 43, Appl
8	4911	100.0	942	4 US-09-883-825-43	Sequence 43, Appl
9	4911	100.0	942	5 PCT-US92-03222-43	Sequence 43, Appl
10	4728.5	96.3	941	1 US-07-872-644-45	Sequence 45, Appl
11	4728.5	96.3	941	1 US-08-297-494-45	Sequence 45, Appl
12	4728.5	96.3	941	1 US-08-297-510-45	Sequence 45, Appl
13	4728.5	96.3	941	1 US-08-479-532-45	Sequence 45, Appl
14	4728.5	96.3	941	1 US-08-455-525-45	Sequence 45, Appl
15	4728.5	96.3	941	1 US-08-455-525-45	Sequence 45, Appl
16	4728.5	96.3	941	3 US-09-139-491-45	Sequence 45, Appl
17	4728.5	96.3	941	4 US-09-883-825-45	Sequence 45, Appl
18	4728.5	96.3	941	4 US-09-708-392-45	Sequence 5, Appl
19	4728.5	96.3	941	4 US-09-949-016-6244	Sequence 6244, Ap
20	4728.5	96.3	941	5 PCT-US92-03222-45	Sequence 45, Appl
21	4657	94.8	921	1 US-07-872-644-39	Sequence 39, Appl
22	4657	94.8	921	1 US-08-297-494-39	Sequence 39, Appl
23	4657	94.8	921	1 US-08-297-510-39	Sequence 39, Appl
24	4657	94.8	921	1 US-08-479-532-39	Sequence 39, Appl
25	4657	94.8	921	1 US-08-455-525-39	Sequence 39, Appl
26	4657	94.8	921	1 US-08-455-525-39	Sequence 39, Appl
27	4657	94.8	921	3 US-09-139-491-39	Sequence 39, Appl

Query Match 100.0% Score 4911; DB 1; Length 942;

28 4657 94.8 921 3 US-09-754-250-5 Sequence 5, Appl  
29 4657 94.8 921 4 US-09-883-825-39 Sequence 39, Appl  
30 4657 94.8 921 5 PCT-US92-03222-39 Sequence 39, Appl  
31 4530.5 92.3 905 3 US-09-754-250-4 Sequence 4, Appl  
32 4474.5 91.1 920 3 US-09-754-250-2 Sequence 2, Appl  
33 3815 77.7 802 4 US-09-949-016-7922 Sequence 7922, Ap  
34 913.5 18.6 779 2 US-08-951-648-6 Sequence 6, Appl  
35 913.5 18.6 779 3 US-09-174-437-6 Sequence 6, Appl  
36 913.5 18.6 779 4 US-09-686-055A-6 Sequence 1, Appl  
37 913.5 18.6 779 4 US-09-420-190-1 Sequence 1, Appl  
38 912 18.6 803 2 US-08-951-648-4 Sequence 4, Appl  
39 912 18.6 803 3 US-09-174-437-4 Sequence 4, Appl  
40 912 18.6 803 4 US-09-686-055A-4 Sequence 4, Appl  
41 911.5 18.6 766 2 US-08-951-648-2 Sequence 2, Appl  
42 911.5 18.6 766 3 US-09-174-437-2 Sequence 2, Appl  
43 911.5 18.6 766 4 US-09-686-055A-2 Sequence 2, Appl  
44 804 16.4 875 1 US-08-480-547A-23 Sequence 23, Appl  
45 804 16.4 875 1 US-08-250-847B-23 Sequence 23, Appl

## ALIGNMENTS

RESULT 1  
US-07-872-644-43  
; Sequence 43, Application US/07872644  
; Patent No. 5389527  
; GENERAL INFORMATION:  
; APPLICANT: Beavo, Joseph A.  
; APPLICANT: Bentley, Kelley  
; APPLICANT: Charbonneau, Harry  
; APPLICANT: Sonnenburg, William K.  
; TITLE OF INVENTION: DNA Encoding Mammalian  
; TITLE OF INVENTION: Phosphodiesterases  
; NUMBER OF SEQUENCES: 58  
; CORRESPONDENCE ADDRESS:  
; ADDRESSEE: Marshall, O'Toole, Gerstein, Murray &  
; ADDRESSEE: Bicknell  
; STREET: Two First National Plaza, 20 South Clark  
; CITY: Chicago  
; STATE: Illinois  
; COUNTRY: USA  
; ZIP: 60603  
; COMPUTER READABLE FORM:  
; MEDIUM TYPE: Floppy disk  
; COMPUTER: IBM PC compatible  
; OPERATING SYSTEM: PC-DOS/MS-DOS  
; SOFTWARE: Patent In Release #1.0, Version #1.25  
; CURRENT APPLICATION DATA:  
; APPLICATION NUMBER: US/07/872,644  
; FILING DATE: 19920420  
; CLASSIFICATION: 435  
; PRIOR APPLICATION DATA:  
; APPLICATION NUMBER: US 07/688,356  
; FILING DATE: 04-APR-1991  
; ATTORNEY/AGENT INFORMATION:  
; NAME: No. 5389527and, Greta E.  
; REGISTRATION NUMBER: 35,302  
; REFERENCE/DOCKET NUMBER: 27866/30822  
; TELECOMMUNICATION INFORMATION:  
; TELEPHONE: (312) 346-5750  
; TELEFAX: (312) 984-9740  
; TELEX: 25-3856  
; INFORMATION FOR SEQ ID NO: 43:  
; SEQUENCE CHARACTERISTICS:  
; LENGTH: 942 amino acids  
; TYPE: AMINO ACID  
; TOPOLOGY: linear  
; MOLECULE TYPE: protein  
US-07-872-644-43

		Best Local Similarity	100.0%;	Pred. No. 0;	Mismatches	0;	Indels	0;	Gaps	0;
		Matches 942; Conservative 0; Mismatches 0; Indels 0; Gaps 0;								
Qy	1	MGQACGHSILCRSQYPAARPAERGGQVFLKPDPEPPPPPCADSLQDALLSLGSLVDV	60							
Db	1	MGQACGHSILCRSQYPAARPAERGGQVFLKPDPEPPPPPCADSLQDALLSLGSLVDV	60							
Qy	61	AGLQAAVKEALSAVLPKVTETVYLLDGESRLVCEPPHELPOEGKVREAVISRKLGN	120							
Db	61	AGLQAAVKEALSAVLPKVTETVYLLDGESRLVCEPPHELPOEGKVREAVISRKLGN	120							
Qy	121	GLGPSDLPGKPLARLAVAPLAPDQVLPVLDKEAGAAVAVILVHCGQLSNEEWSLOAV	180							
Db	121	GLGPSDLPGKPLARLAVAPLAPDQVLPVLDKEAGAAVAVILVHCGQLSNEEWSLOAV	180							
Qy	181	EKHTLVALKRVQALQORESSVAPEATQNPPEAAGDQGGVAYTDQDRKILQCGELYDL	240							
Db	181	EKHTLVALKRVQALQORESSVAPEATQNPPEAAGDQGGVAYTDQDRKILQCGELYDL	240							
Qy	241	DASSLQKLVQLQOETQASRCCLLVSEDNLQLSCKVIGDKVLEEEISFPLTTGRLQGV	300							
Db	241	DASSLQKLVQLQOETQASRCCLLVSEDNLQLSCKVIGDKVLEEEISFPLTTGRLQGV	300							
Qy	301	VEDKKSILQKDLTSEDMDQQLSMLGCEVQAMLCVPVISRATDQVVALACAFNKLGGDLFT	360							
Db	301	VEDKKSILQKDLTSEDMDQQLSMLGCEVQAMLCVPVISRATDQVVALACAFNKLGGDLFT	360							
Qy	361	DQDEHVIQHCFTYSTVLTSTLAFQEQKLCQEQALLQVAKNLFTHLDDVSVLLQEIIT	420							
Db	361	DQDEHVIQHCFTYSTVLTSTLAFQEQKLCQEQALLQVAKNLFTHLDDVSVLLQEIIT	420							
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Db	421	EARNLSNAEICSVFLLDQNEILVAKVFDGCVVEDESYEIRIPADQGIAGHVATTGQILNIP	480							
Qy	481	DAYAHLFYRGVDDSTGFRTRNLCFPIKNEQEVIGVAELVNKINGPWFSKFDEDLATA	540							
Db	481	DAYAHLFYRGVDDSTGFRTRNLCFPIKNEQEVIGVAELVNKINGPWFSKFDEDLATA	540							
Qy	541	FSIYCGISIAHSLLYKKVNEAQYRSHLANEMMYHMKVSDDEYTKLLHDGIQPVAAIDSN	600							
Db	541	FSIYCGISIAHSLLYKKVNEAQYRSHLANEMMYHMKVSDDEYTKLLHDGIQPVAAIDSN	600							
Qy	601	FASFTYTPRSIPEDDTSNAILSMLODMFNINNYKIDCPTLARFCILMVKKGYRDPYHNMW	660							
Db	601	FASFTYTPRSIPEDDTSNAILSMLODMFNINNYKIDCPTLARFCILMVKKGYRDPYHNMW	660							
Qy	661	HAFVSVHFCYLLYKNLELTNYLEDMEIFALFISCMCHDLDRGTNNSPQVASKSVLAALY	720							
Db	661	HAFVSVHFCYLLYKNLELTNYLEDMEIFALFISCMCHDLDRGTNNSPQVASKSVLAALY	720							
Qy	721	SSEGSVMRHHFAQAIALINTHGNCNIPHFGRKQYQRMILMDRDIILATDLAHLRIPKD	780							
Db	721	SSEGSVMRHHFAQAIALINTHGNCNIPHFGRKQYQRMILMDRDIILATDLAHLRIPKD	780							
Qy	781	LQKMAEVGYDRTNKHSHLLCLLMTSCDLSQDTKGWKTTRKIAELIYKEFFSQGDLEKA	840							
Db	781	LQKMAEVGYDRTNKHSHLLCLLMTSCDLSQDTKGWKTTRKIAELIYKEFFSQGDLEKA	840							
Qy	841	MGNRPMEWMDEKAYIPELOISFMEHIAMPYKLLQDLFPKAAELYERVASNRHWTKVS	900							
Db	841	MGNRPMEWMDEKAYIPELOISFMEHIAMPYKLLQDLFPKAAELYERVASNRHWTKVS	900							
Qy	901	HKFTIRGLPSNNSLDFLDEEVEVPLDGCARAPINGCCSLDAE	942							
Db	901	HKFTIRGLPSNNSLDFLDEEVEVPLDGCARAPINGCCSLDAE	942							

RESULT 2

US-08-297-494-43  
; Sequence 43, Application US/08297494  
; Patent No. 5580771  
; GENERAL INFORMATION:

; APPLICANT: Beavo, Joseph A.  
; APPLICANT: Bentley, Kelley  
; APPLICANT: Charbonneau, Harry  
; APPLICANT: Sonnenburg, William K.  
; TITLE OF INVENTION: DNA Encoding Mammalian  
; TITLE OF INVENTION: Phosphodiesterases  
; NUMBER OF SEQUENCES: 58  
; CORRESPONDENCE ADDRESS:  
; ADDRESSEE: Marshall, O'Toole, Gerstein, Murray &  
; ADDRESSEE: Bicknell  
; STREET: Two First National Plaza, 20 South Clark  
; STREET: Street  
; CITY: Chicago  
; STATE: Illinois  
; COUNTRY: USA  
; ZIP: 60603  
; COMPUTER READABLE FORM:  
; MEDIUM TYPE: Floppy disk  
; COMPUTER: IBM PC compatible  
; OPERATING SYSTEM: PC-DOS/MS-DOS  
; SOFTWARE: Patent in Release #1.0, Version #1.25  
; CURRENT APPLICATION DATA:  
; APPLICATION NUMBER: US/08/297,494  
; FILING DATE:  
; CLASSIFICATION: 435  
; PRIOR APPLICATION DATA:  
; APPLICATION NUMBER: US 07/688,356  
; FILING DATE: 04-APR-1991  
; ATTORNEY/AGENT INFORMATION:  
; NAME: No. 5580771and, Greta E.  
; REGISTRATION NUMBER: 35,302  
; REFERENCE/DOCKET NUMBER: 27866/30822  
; TELECOMMUNICATION INFORMATION:  
; TELEPHONE: (312) 346-5750  
; TELEFAX: (312) 984-9740  
; TELEX: 25-3856  
; INFORMATION FOR SEQ ID NO: 43:  
; SEQUENCE CHARACTERISTICS:  
; LENGTH: 942 amino acids  
; TYPE: amino acid  
; TOPOLOGY: linear  
; MOLECULE TYPE: protein  
; US-08-297-494-43

Query Match 100.0%; Score 4911; DB 1; Length 942;  
Best Local Similarity 100.0%; Pred. No. 0;  
Matches 942; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy	1	MGQACGHSILCRSQYPAARPAERGGQVFLKPDPEPPPPPCADSLQDALLSLGSLVDV	60
Db	1	MGQACGHSILCRSQYPAARPAERGGQVFLKPDPEPPPPPCADSLQDALLSLGSLVDV	60
Qy	61	AGLQAAVKEALSAVLPKVTETVYLLDGESRLVCEPPHELPOEGKVREAVISRKLGN	120
Db	61	AGLQAAVKEALSAVLPKVTETVYLLDGESRLVCEPPHELPOEGKVREAVISRKLGN	120
Qy	121	GLGPSDLPGKPLARLAVAPLAPDQVLPVLDKEAGAAVAVILVHCGQLSNEEWSLOAV	180
Db	121	GLGPSDLPGKPLARLAVAPLAPDQVLPVLDKEAGAAVAVILVHCGQLSNEEWSLOAV	180
Qy	181	EKHTLVALKRVQALQORESSVAPEATQNPPEAAGDQGGVAYTDQDRKILQCGELYDL	240
Db	181	EKHTLVALKRVQALQORESSVAPEATQNPPEAAGDQGGVAYTDQDRKILQCGELYDL	240
Qy	241	DASSLQKLVQLQOETQASRCCLLVSEDNLQLSCKVIGDKVLEEEISFPLTTGRLQGV	300
Db	241	DASSLQKLVQLQOETQASRCCLLVSEDNLQLSCKVIGDKVLEEEISFPLTTGRLQGV	300
Qy	301	VEDKKSILQKDLTSEDMDQQLSMLGCEVQAMLCVPVISRATDQVVALACAFNKLGGDLFT	360
Db	301	VEDKKSILQKDLTSEDMDQQLSMLGCEVQAMLCVPVISRATDQVVALACAFNKLGGDLFT	360
Qy	361	DQDEHVIQHCFTYSTVLTSTLAFQEQKLCQEQALLQVAKNLFTHLDDVSVLLQEIIT	420



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Db 361 DQDEHVIQCHFYTSVLTSTLAFOKEQKLCCEQALLQVAKNLFTHLDDVSVLLQEIIT 420
Qy 421 EARNLSNABICSVFLDDQNELVAKVFDGGVDESEYIIRIPADQGIAGHVATTGQILNIP 480
Db 421 EARNLSNABICSVFLDDQNELVAKVFDGGVDESEYIIRIPADQGIAGHVATTGQILNIP 480
Qy 481 DAYAHLPLFYRGVDDSTGFRTRNLCFPIKNEQVIGVAELVKNKINGPWFSEKDEDLATA 540
Db 481 DAYAHLPLFYRGVDDSTGFRTRNLCFPIKNEQVIGVAELVKNKINGPWFSEKDEDLATA 540
Qy 541 FSIYCGISIAHSLLYKKNVNAQYRSHLANEMMYHMKVSDDEYTKLLHDIOPVAAIDSN 600
Db 541 FSIYCGISIAHSLLYKKNVNAQYRSHLANEMMYHMKVSDDEYTKLLHDIOPVAAIDSN 600
Qy 601 FASFTYTPRSLPEDDTSMAILSMLQDMNFINNYKIDCPTLARFCLMVKGYRDPVYHNM 660
Db 601 FASFTYTPRSLPEDDTSMAILSMLQDMNFINNYKIDCPTLARFCLMVKGYRDPVYHNM 660
Qy 661 HAFVSVSHFCYLLYKNLETNYLEDEMEIFALFISCMCHDLHRTGNTNNSFOVASKSVLAALY 720
Db 661 HAFVSVSHFCYLLYKNLETNYLEDEMEIFALFISCMCHDLHRTGNTNNSFOVASKSVLAALY 720
Qy 721 SSEGSMERHHFAQAIAIINTHGCNIFDHFSSKDYQRMULDLMRDIIILATDLAHLRIFKD 780
Db 721 SSEGSMERHHFAQAIAIINTHGCNIFDHFSSKDYQRMULDLMRDIIILATDLAHLRIFKD 780
Qy 781 LQKMAEVGYDRTNKHSHLLCLLMTSCDLSQDTGKWKTRKIAELIYKEFFSQGDLEKA 840
Db 781 LQKMAEVGYDRTNKHSHLLCLLMTSCDLSQDTGKWKTRKIAELIYKEFFSQGDLEKA 840
Qy 841 MGNRPMEMMDREKAVIPELQISFMEHIAMPIYKLLQDLFPKAAELYERVASNREHWTKVS 900
Db 841 MGNRPMEMMDREKAVIPELQISFMEHIAMPIYKLLQDLFPKAAELYERVASNREHWTKVS 900
Qy 901 HKFTIRGLPSNNSLDFDEYEVPLDGGARAPINGCCSLDAE 942
Db 901 HKFTIRGLPSNNSLDFDEYEVPLDGGARAPINGCCSLDAE 942
```

## RESULT 3

```
US-08-297-510-43
; Sequence 43, Application US/08297510
; Patent No. 5602019
; GENERAL INFORMATION:
; APPLICANT: Beavo, Joseph A.
; APPLICANT: Bentley, Kelley
; APPLICANT: Charbonneau, Harry
; APPLICANT: Sonnenburg, William K.
; TITLE OF INVENTION: DNA Encoding Mammalian
; TITLE OF INVENTION: Phosphodiesterases
; NUMBER OF SEQUENCES: 58
; CORRESPONDENCE ADDRESSES:
; ADDRESSEE: Marshall, O'Toole, Gerstein, Murray &
; ADDRESSEE: Bicknell
; STREET: Two First National Plaza, 20 South Clark
; CITY: Chicago
; STATE: Illinois
; COUNTRY: USA
; ZIP: 60603
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patent In Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/297,510
; FILING DATE:
; CLASSIFICATION: 435
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 07/688,356
; FILING DATE: 04-APR-1991
```

```
; ATTORNEY/AGENT INFORMATION:
; NAME: No. 5602019and, Greta E.
; REGISTRATION NUMBER: 35,302
; REFERENCE/DOCKET NUMBER: 27866/30822
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (312) 346-5750
; TELEFAX: (312) 984-9740
; TELEX: 25-3856
; INFORMATION FOR SEQ ID NO: 43:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 942 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: protein
; US-08-297-510-43

Query Match 100.0%; Score 4911; DB 1; Length 942;
Best Local Similarity 100.0%; Pred. No. 0;
Matches 942; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 MQQACGHSILCSQQYPAARPAERGGQVFLKPDPPPPPPQCADSLQDALLSLGSDIV 60
Db 1 MQQACGHSILCSQQYPAARPAERGGQVFLKPDPPPPPPQCADSLQDALLSLGSDIV 60
Qy 61 AGLOQAVKEALSAVLPKVTETVYLLDGSRLVCEPPHPELPOEGKVRKAVISRKELGCN 120
Db 61 AGLOQAVKEALSAVLPKVTETVYLLDGSRLVCEPPHPELPOEGKVRKAVISRKELGCN 120
Qy 121 GUGPSDLQPKPLARLAVPLAPDQVILVPLVDKEAGAAVILVHCGQLSDNEEWSLQAV 180
Db 121 GUGPSDLQPKPLARLAVPLAPDQVILVPLVDKEAGAAVILVHCGQLSDNEEWSLQAV 180
Qy 181 EKHTLVALKRVQALQRESSVAPEATQNPPEEAAGDQKGVAYTQDQRKILQLCGELYDL 240
Db 181 EKHTLVALKRVQALQRESSVAPEATQNPPEEAAGDQKGVAYTQDQRKILQLCGELYDL 240
Qy 241 DASSLQLKVLQVLOQETOASRCCLLVSEDNIQLSKVIGDKVLEBEISFPLTTGRGQV 300
Db 241 DASSLQLKVLQVLOQETOASRCCLLVSEDNIQLSKVIGDKVLEBEISFPLTTGRGQV 300
Qy 301 VEDKESIQLKDLTSEDMOQLSMLGCEVQAMLCVPISRATQVQVALACAFNKGGLFT 360
Db 301 VEDKESIQLKDLTSEDMOQLSMLGCEVQAMLCVPISRATQVQVALACAFNKGGLFT 360
Qy 361 DQDEHVIQCHFYTSVLTSTLAFOKEQKLCCEQALLQVAKNLFTHLDDVSVLLQEIIT 420
Db 361 DQDEHVIQCHFYTSVLTSTLAFOKEQKLCCEQALLQVAKNLFTHLDDVSVLLQEIIT 420
Qy 421 EARNLSNABICSVFLDDQNELVAKVFDGGVDESEYIIRIPADQGIAGHVATTGQILNIP 480
Db 421 EARNLSNABICSVFLDDQNELVAKVFDGGVDESEYIIRIPADQGIAGHVATTGQILNIP 480
Qy 481 DAYAHLPLFYRGVDDSTGFRTRNLCFPIKNEQVIGVAELVKNKINGPWFSEKDEDLATA 540
Db 481 DAYAHLPLFYRGVDDSTGFRTRNLCFPIKNEQVIGVAELVKNKINGPWFSEKDEDLATA 540
Qy 541 FSIYCGISIAHSLLYKKNVNAQYRSHLANEMMYHMKVSDDEYTKLLHDIOPVAAIDSN 600
Db 541 FSIYCGISIAHSLLYKKNVNAQYRSHLANEMMYHMKVSDDEYTKLLHDIOPVAAIDSN 600
Qy 601 FASFTYTPRSLPEDDTSMAILSMLQDMNFINNYKIDCPTLARFCLMVKGYRDPVYHNM 660
Db 601 FASFTYTPRSLPEDDTSMAILSMLQDMNFINNYKIDCPTLARFCLMVKGYRDPVYHNM 660
Qy 661 HAFVSVSHFCYLLYKNLETNYLEDEMEIFALFISCMCHDLHRTGNTNNSFOVASKSVLAALY 720
Db 661 HAFVSVSHFCYLLYKNLETNYLEDEMEIFALFISCMCHDLHRTGNTNNSFOVASKSVLAALY 720
Qy 721 SSEGSMERHHFAQAIAIINTHGCNIFDHFSSKDYQRMULDLMRDIIILATDLAHLRIFKD 780
Db 721 SSEGSMERHHFAQAIAIINTHGCNIFDHFSSKDYQRMULDLMRDIIILATDLAHLRIFKD 780
Qy 781 LQKMAEVGYDRTNKHSHLLCLLMTSCDLSQDTGKWKTRKIAELIYKEFFSQGDLEKA 840
```

Db 781 LQKMAEYGYDRTNKHSHLLCLLMTSCDLSQDTKGWKTTRKIAELIYKEFFSQGDLKA 840  
Qy 841 MGNRPMMMDREKAYIPBLQISFMEHTAMPIYKLLQDLFPKAAELYERVASNRHWTKVS 900  
Db 841 MGNRPMMMDREKAYIPBLQISFMEHTAMPIYKLLQDLFPKAAELYERVASNRHWTKVS 900  
Qy 901 HKFTIRGLPSNNSLDFLDEEYVDPDLCARAPINGCCSLDAE 942  
Db 901 HKFTIRGLPSNNSLDFLDEEYVDPDLCARAPINGCCSLDAE 942

## RESULT 4

US-08-479-532-43  
; Sequence 43, Application US/08479532  
; Patent No. 576752  
; GENERAL INFORMATION:  
; APPLICANT: Beavo, Joseph A.  
; APPLICANT: Bentley, Kelley  
; APPLICANT: Charbonneau, Harry  
; APPLICANT: Sonnenburg, William K.  
; TITLE OF INVENTION: DNA Encoding Mammalian  
; TITLE OF INVENTION: Phosphodiesterases  
; NUMBER OF SEQUENCES: 58  
; CORRESPONDENCE ADDRESS:  
; ADDRESSEE: Marshall, O'Toole, Gerstein, Murray &  
; ADDRESSEE: Bicknell  
; STREET: Two First National Plaza, 20 South Clark  
; CITY: Chicago  
; STATE: Illinois  
; COUNTRY: USA  
; ZIP: 60603  
; COMPUTER READABLE FORM:  
; MEDIUM TYPE: Floppy disk  
; COMPUTER: IBM PC compatible  
; OPERATING SYSTEM: PC-DOS/MS-DOS  
; SOFTWARE: Patent In Release #1.0, Version #1.25  
; CURRENT APPLICATION DATA:  
; APPLICATION NUMBER: US/08/479,532  
; FILING DATE: 07-JUN-1995  
; CLASSIFICATION: 435  
; PRIOR APPLICATION DATA:  
; APPLICATION NUMBER: 08/297,494  
; FILING DATE:  
; APPLICATION NUMBER: US 07/688,356  
; FILING DATE: 04-APR-1991  
; ATTORNEY/AGENT INFORMATION:  
; NAME: No. 576752and, Greta E.  
; REGISTRATION NUMBER: 35,302  
; REFERENCE/DOCKET NUMBER: 27866/30822  
; TELECOMMUNICATION INFORMATION:  
; TELEPHONE: (312) 346-5750  
; TELEFAX: (312) 984-9740  
; TELEX: 25-3856  
; INFORMATION FOR SEQ ID NO: 43:  
; SEQUENCE CHARACTERISTICS:  
; LENGTH: 942 amino acids  
; TYPE: amino acid  
; TOPOLOGY: linear  
; MOLECULE TYPE: protein  
; US-08-479-532-43

Query Match 100.0%; Score 4911; DB 1; Length 942;  
Best Local Similarity 100.0%; Pred. No. 0;  
Matches 942; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
Qy 1 MGQACGHSILCRSQYPAARPAERGGQVFLKPDDEPPPPPPQPCADSLQDALLSLGSDIV 60  
Db 1 MGQACGHSILCRSQYPAARPAERGGQVFLKPDDEPPPPPPQPCADSLQDALLSLGSDIV 60  
Qy 61 AGLQQAQVEALSAVLPKVETVYTYLLDGSRLVCEPPEHPHQSGKRVAVISRKLGCN 120

Db 61 AGLQQAQVEALSAVLPKVETVYTYLLDGSRLVCEPPEHPHQSGKRVAVISRKLGCN 120  
Qy 121 GLGPSDLPGKPLARLVAFLAPDQTVIPLVDKAGAAVAIVLHVCQGLSNEWSLQAV 180  
Db 121 GLGPSDLPGKPLARLVAFLAPDQTVIPLVDKAGAAVAIVLHVCQGLSNEWSLQAV 180  
Qy 181 EKHTLVALKRVQALQORESSVAPETONPPPEAAGDQGGVAYTDQDKILQLCGELYDL 240  
Db 181 EKHTLVALKRVQALQORESSVAPETONPPPEAAGDQGGVAYTDQDKILQLCGELYDL 240  
Qy 241 DASSLQQLKVLQYLAQETQASRCCLLLVSEDNQLQSKVIGDKVLEEEISFPLTTRGLQGV 300  
Db 241 DASSLQQLKVLQYLAQETQASRCCLLLVSEDNQLQSKVIGDKVLEEEISFPLTTRGLQGV 300  
Qy 301 VEDKKSITQLKDLTSEDNQLOSLMGCEVQAMLCVPVISRATDQVVALACAFNKLGGLFT 360  
Db 301 VEDKKSITQLKDLTSEDNQLOSLMGCEVQAMLCVPVISRATDQVVALACAFNKLGGLFT 360  
Qy 361 DQDEHVIQCHFHVTSTVLSTLAFQKQKLCCEQALLQVAKNLFTHLDDVSVLLQEIIT 420  
Db 361 DQDEHVIQCHFHVTSTVLSTLAFQKQKLCCEQALLQVAKNLFTHLDDVSVLLQEIIT 420  
Qy 421 EARNLSNAEICSVFLLDQNELVAKVFDGQVVEDESYEIRIPADQGIAGHVATTGQILNIP 480  
Db 421 EARNLSNAEICSVFLLDQNELVAKVFDGQVVEDESYEIRIPADQGIAGHVATTGQILNIP 480  
Qy 481 DAYAHLPLFYRGVDDSTGFRTRNLCFPIKQENQVIGVAELVNKINGWFSKFDLATA 540  
Db 481 DAYAHLPLFYRGVDDSTGFRTRNLCFPIKQENQVIGVAELVNKINGWFSKFDLATA 540  
Qy 541 FSIYCGISIAHSLLYKKVNEAQYRSHLANEMMMTHMKVSDDEYTKLHDGQPVAAIDSN 600  
Db 541 FSIYCGISIAHSLLYKKVNEAQYRSHLANEMMMTHMKVSDDEYTKLHDGQPVAAIDSN 600  
Qy 601 FASFTYTPRSIPEDDTSMAILSMQDMNFNNYKIDCPTTLARFCLMVKKGYRDPYHNWM 660  
Db 601 FASFTYTPRSIPEDDTSMAILSMQDMNFNNYKIDCPTTLARFCLMVKKGYRDPYHNWM 660  
Qy 661 HAFSVSHFCYLLYKNLELTNYLEDMEIFALPISCMCHDLHRGTNNNSFQVASKSVLAALY 720  
Db 661 HAFSVSHFCYLLYKNLELTNYLEDMEIFALPISCMCHDLHRGTNNNSFQVASKSVLAALY 720  
Qy 721 SSEGSMVRRHFAQAIALLNTHGNCIFDHFSRKYQRMQLMRDIIILATDLAHLRIKPD 780  
Db 721 SSEGSMVRRHFAQAIALLNTHGNCIFDHFSRKYQRMQLMRDIIILATDLAHLRIKPD 780  
Qy 781 LQKMAEYGYDRTNKHSHLLCLLMTSCDLSQDTKGWKTTRKIAELIYKEFFSQGDLKA 840  
Db 781 LQKMAEYGYDRTNKHSHLLCLLMTSCDLSQDTKGWKTTRKIAELIYKEFFSQGDLKA 840  
Qy 841 MGNRPMMMDREKAYIPBLQISFMEHTAMPIYKLLQDLFPKAAELYERVASNRHWTKVS 900  
Db 841 MGNRPMMMDREKAYIPBLQISFMEHTAMPIYKLLQDLFPKAAELYERVASNRHWTKVS 900  
Qy 901 HKFTIRGLPSNNSLDFLDEEYVDPDLCARAPINGCCSLDAE 942  
Db 901 HKFTIRGLPSNNSLDFLDEEYVDPDLCARAPINGCCSLDAE 942

## RESULT 5

US-08-455-526-43  
; Sequence 43, Application US/08455526  
; Patent No. 5789553  
; GENERAL INFORMATION:  
; APPLICANT: Beavo, Joseph A.  
; APPLICANT: Bentley, Kelley  
; APPLICANT: Charbonneau, Harry  
; APPLICANT: Sonnenburg, William K.  
; TITLE OF INVENTION: DNA Encoding Mammalian  
; TITLE OF INVENTION: Phosphodiesterases  
; NUMBER OF SEQUENCES: 58  
; CORRESPONDENCE ADDRESS:  
; ADDRESSEE: Marshall, O'Toole, Gerstein, Murray &

ADDRESSEE: Bicknell  
STREET: Two First National Plaza, 20 South Clark  
CITY: Chicago  
STATE: Illinois  
COUNTRY: USA  
ZIP: 60603  
COMPUTER READABLE FORM:  
MEDIUM TYPE: Floppy disk  
COMPUTER: IBM PC compatible  
OPERATING SYSTEM: PC-DOS/MS-DOS  
SOFTWARE: Patent In Release #1.0, Version #1.25  
CURRENT APPLICATION DATA:  
FILING DATE: 04-APR-1991  
FILING DATE: 31-MAY-1995  
CLASSIFICATION: 530  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: US 08/297,494  
FILING DATE: 29-AUG-1994  
APPLICATION NUMBER: US 07/688,356  
FILING DATE: 04-APR-1991  
ATTORNEY/AGENT INFORMATION:  
NAME: No. 5789553and, Greta E.  
REGISTRATION NUMBER: 35,302  
REFERENCE/DOCKET NUMBER: 27866/30822  
TELEPHONE: (312) 346-5750  
TELEFAX: (312) 984-9740  
TELEX: 25-3856  
INFORMATION FOR SEQ ID NO: 43:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 942 amino acids  
TYPE: amino acid  
TOPOLOGY: linear  
MOLECULE TYPE: protein  
US-08-455-526-43

Query Match 100.0%; Score 4911; DB 1; Length 942;  
Best Local Similarity 100.0%; Pred. No. 0;  
Matches 942; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 MQACGHSILCSQQYPAARPAEPGRQQVFLKPDPEPPPPQPCADSLQDALLSLGSDIV 60  
DB 1 MQACGHSILCSQQYPAARPAEPGRQQVFLKPDPEPPPPQPCADSLQDALLSLGSDIV 60

QY 61 AGLOQAVKEALSAPVKVETVYLLDGSRLVCEPPEPHELPOEGKGVREAVISRKLGN 120  
DB 61 AGLOQAVKEALSAPVKVETVYLLDGSRLVCEPPEPHELPOEGKGVREAVISRKLGN 120

QY 121 GLGPSDLPGKPLARLVAPLAPDTQVLVPLVDKEAGAAVILVHCGQLSDNEEWSLOAV 180  
DB 121 GLGPSDLPGKPLARLVAPLAPDTQVLVPLVDKEAGAAVILVHCGQLSDNEEWSLOAV 180

QY 181 EKHTLVAKRVQALQORESSVAPEATQNPPEAAGDQKGVAYTDQDRKILQCGELYDL 240  
DB 181 EKHTLVAKRVQALQORESSVAPEATQNPPEAAGDQKGVAYTDQDRKILQCGELYDL 240

QY 241 DASSILQKVLQOETQASRCCLLVSDNLQSKVIGDKVLEEEISFPLTTGRLGQV 300  
DB 241 DASSILQKVLQOETQASRCCLLVSDNLQSKVIGDKVLEEEISFPLTTGRLGQV 300

QY 301 VEDKKSILQKLTSEDMDQQLGMLGCEVQAMLCVPVISRATDQVVALACAFNKGDLFT 360  
DB 301 VEDKKSILQKLTSEDMDQQLGMLGCEVQAMLCVPVISRATDQVVALACAFNKGDLFT 360

QY 361 DQDEHVIQCHFYHTSVLTSTLAFQKEQKLCCEQALLQVAKNLFTHLDDVSVLQEIIT 420  
DB 361 DQDEHVIQCHFYHTSVLTSTLAFQKEQKLCCEQALLQVAKNLFTHLDDVSVLQEIIT 420

QY 421 EARNLSNABICSVFLDDQNELVAKVFDGGVVEDESYEIRIPADQGIAGHVATTGILNIP 480  
DB 421 EARNLSNABICSVFLDDQNELVAKVFDGGVVEDESYEIRIPADQGIAGHVATTGILNIP 480

QY 481 DAYAHLFYRGVDDSTGFRTRNLCFPKIKENQEVIGVAELVKNKINGPWFSKFDEDLATA 540  
DB 481 DAYAHLFYRGVDDSTGFRTRNLCFPKIKENQEVIGVAELVKNKINGPWFSKFDEDLATA 540

QY 541 FSIYCGISIAHSLLYKKVNEAQYRSHLANEMMYHMKVSDDEYTKLLHDGIGQVAAIDSN 600  
DB 541 FSIYCGISIAHSLLYKKVNEAQYRSHLANEMMYHMKVSDDEYTKLLHDGIGQVAAIDSN 600

QY 601 FASFTYTPRSLPEDDTSMAILSMLQDMNFNNYKIDCPTLARFCLMVKGYRDPYPYHNM 660  
DB 601 FASFTYTPRSLPEDDTSMAILSMLQDMNFNNYKIDCPTLARFCLMVKGYRDPYPYHNM 660

QY 661 HAFVSVSHFCYLLYKNELETNYLEDMEIFALFISCHDLDRGTNNSPQVASKSVLAALY 720  
DB 661 HAFVSVSHFCYLLYKNELETNYLEDMEIFALFISCHDLDRGTNNSPQVASKSVLAALY 720

QY 721 SSEGSVMERHHPAQAIJLNTHGNCIFDHFGRKDYQRMDLMDRIILATDLAHLRIFKD 780  
DB 721 SSEGSVMERHHPAQAIJLNTHGNCIFDHFGRKDYQRMDLMDRIILATDLAHLRIFKD 780

QY 781 LQKMAEVGYDRTNKQHSLLCLLMTSCDLSQTKGWKTRKIAELIYKEFFSQGDLEKA 840  
DB 781 LQKMAEVGYDRTNKQHSLLCLLMTSCDLSQTKGWKTRKIAELIYKEFFSQGDLEKA 840

QY 841 MGNRPMMMDREKAYIPELQISFMEHIAPIYKLLQDLPPKAAELYERVASNREHWTKVS 900  
DB 841 MGNRPMMMDREKAYIPELQISFMEHIAPIYKLLQDLPPKAAELYERVASNREHWTKVS 900

QY 901 HKFTIRGLPSNNSLDPLDEEYEVDPDLCGARAPINGCCSLDAE 942  
DB 901 HKFTIRGLPSNNSLDPLDEEYEVDPDLCGARAPINGCCSLDAE 942

RESULT 6

US-08-455-525-43  
Sequence 43, Application US/08455525  
Patent No. 5800987  
GENERAL INFORMATION:  
APPLICANT: Beavo, Joseph A.  
APPLICANT: Bentley, Kelley  
APPLICANT: Charbonneau, Harry  
APPLICANT: Sonnenburg, William K.  
TITLE OF INVENTION: DNA Encoding Mammalian  
NUMBER OF SEQUENCES: 58  
CORRESPONDENCE ADDRESS:  
ADDRESSEE: Marshall, O'Toole, Gerstein, Murray &  
ADDRESSEE: Bicknell  
STREET: Two First National Plaza, 20 South Clark  
CITY: Chicago  
STATE: Illinois  
COUNTRY: USA  
ZIP: 60603  
COMPUTER READABLE FORM:  
MEDIUM TYPE: Floppy disk  
COMPUTER: IBM PC compatible  
OPERATING SYSTEM: PC-DOS/MS-DOS  
SOFTWARE: Patent In Release #1.0, Version #1.25  
CURRENT APPLICATION DATA:  
FILING DATE: 31-MAY-1995  
CLASSIFICATION: 435  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: 08/297,494  
FILING DATE:  
APPLICATION NUMBER: US 07/688,356  
FILING DATE: 04-APR-1991  
ATTORNEY/AGENT INFORMATION:  
NAME: No. 5800987and, Greta E.  
REGISTRATION NUMBER: 35,302  
REFERENCE/DOCKET NUMBER: 27866/30822  
TELECOMMUNICATION INFORMATION:



121 GLGPSDLPGKPLARLVAPLADPTQVLVPLVDKEGAVAAVILVHCGQLSDNEWSLQAV 180  
181 EKHTLVALKRVQALQORESSVAPEATQNPPEBAAGDQKGGVAYTQDQRKILQLCGELYDL 240  
181 EKHTLVALKRVQALQORESSVAPEATQNPPEBAAGDQKGGVAYTQDQRKILQLCGELYDL 240  
241 DASSLQKLVQYLOQETOASRCCLLVSDNQLQSKVIGDKVLEBEEISFPITTRGLQGV 300  
241 DASSLQKLVQYLOQETOASRCCLLVSDNQLQSKVIGDKVLEBEEISFPITTRGLQGV 300  
301 VEDKKSIOQLKDLTSEDQMLQSMGCEVQMLCVPISRATQVVALACAFNKLGGDLFT 360  
301 VEDKKSIOQLKDLTSEDQMLQSMGCEVQMLCVPISRATQVVALACAFNKLGGDLFT 360  
361 DQDEHVIQHCFTYTSVLTLSTLAFQKEQKLCCEQALLQVAKNLFTHLDDVSVLQEIIT 420  
361 DQDEHVIQHCFTYTSVLTLSTLAFQKEQKLCCEQALLQVAKNLFTHLDDVSVLQEIIT 420  
421 EARNLSNABICSVFLLDQNELVAKVFDGGVDESYEIRIPADQGIAGHVATTGQILNIP 480  
421 EARNLSNABICSVFLLDQNELVAKVFDGGVDESYEIRIPADQGIAGHVATTGQILNIP 480  
481 DAYAHLPLFVRGVDSTGFRTRNLCPPIKVENQEVIGVLAELVKNKINGPWFSEFDEDLATA 540  
481 DAYAHLPLFVRGVDSTGFRTRNLCPPIKVENQEVIGVLAELVKNKINGPWFSEFDEDLATA 540  
541 PSYICGISTAHSLLYKKNVNEAQRSHLANEMMMYHMKVSDDEYTKLLHDGIOPVAAIDSN 600  
541 PSYICGISTAHSLLYKKNVNEAQRSHLANEMMMYHMKVSDDEYTKLLHDGIOPVAAIDSN 600  
601 PASFTYTPRSLPDDTSMALLSMLQDMNFINNYKIDCPTLARFCLMVKKGYRDPYHNMM 660  
601 PASFTYTPRSLPDDTSMALLSMLQDMNFINNYKIDCPTLARFCLMVKKGYRDPYHNMM 660  
661 HAFVSVHFCYLLYKNLELNYLEDMEIFALFISCMCHDLDRGTNNNSFOVASKSVLAALY 720  
661 HAFVSVHFCYLLYKNLELNYLEDMEIFALFISCMCHDLDRGTNNNSFOVASKSVLAALY 720  
721 SSEGSMERHFAQAIAILNTHGNCIFDHSRKYORMLDMLDRDIIILATDLAHLRIKPD 780  
721 SSEGSMERHFAQAIAILNTHGNCIFDHSRKYORMLDMLDRDIIILATDLAHLRIKPD 780  
781 LQKMAEVGYDRNTKQHSLLCLLMTSCDLSQDTGKWKTRKIAELIYKEFFSQGDLEKA 840  
781 LQKMAEVGYDRNTKQHSLLCLLMTSCDLSQDTGKWKTRKIAELIYKEFFSQGDLEKA 840  
841 MGNRRPMEMMDREKAVIPELQISFMEHIAMPIYKLLQDLPPKAAELYERVASNRHWTKVS 900  
841 MGNRRPMEMMDREKAVIPELQISFMEHIAMPIYKLLQDLPPKAAELYERVASNRHWTKVS 900  
901 HKFTIRGLPSNNSLDFLDEYEVDPDLGARABINGCCSLDAE 942  
901 HKFTIRGLPSNNSLDFLDEYEVDPDLGARABINGCCSLDAE 942

RESULT 8

US-09-883-825-43  
Sequence 43, Application US/09883825  
Patent No. 6642040

GENERAL INFORMATION:

APPLICANT: Beavo, Joseph A.  
Bentley, Kelley  
Charbonneau, Harry  
Sonnenburg, William K.  
TITLE OF INVENTION: DNA Encoding Mammalian  
Phosphodiesterases  
NUMBER OF SEQUENCES: 58  
CORRESPONDENCE ADDRESS:  
ADDRESSEE: Marshall, O'Toole, Gerstein, Murray &  
Bicknell  
STREET: Two First National Plaza, 20 South Clark  
Street

CITY: Chicago  
STATE: Illinois  
COUNTRY: USA  
ZIP: 60603  
COMPUTER READABLE FORM:  
MEDIUM TYPE: Floppy disk  
COMPUTER: IBM PC compatible  
OPERATING SYSTEM: PC-DOS/MS-DOS  
SOFTWARE: Patent In Release #1.0, Version #1.25  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/09/883,825  
FILING DATE: 18-Jun-2001  
CLASSIFICATION: <Unknown>  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: 09/123,783  
FILING DATE: <Unknown>  
APPLICATION NUMBER: 08/297,494  
FILING DATE: <Unknown>  
APPLICATION NUMBER: US 07/688,356  
FILING DATE: 04-APR-1991  
ATTORNEY/AGENT INFORMATION:  
NAME: No. 6642040and, Greta E.  
REGISTRATION NUMBER: 35,302  
REFERENCE/DOCKET NUMBER: 27866/30822  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: (312) 346-5750  
TELEFAX: (312) 984-9740  
TELEX: 25-3856  
INFORMATION FOR SEQ ID NO: 43:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 942 amino acids  
TYPE: amino acid  
TOPOLOGY: linear  
MOLECULE TYPE: protein  
SEQUENCE DESCRIPTION: SEQ ID NO: 43:  
US-09-883-825-43

Query Match 100.0%; Score 4911; DB 4; Length 942;  
Best Local Similarity 100.0%; Pred. No. 0;  
Matches 942; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 MQAGCHSILCRSQYPAARPAEPGRQQVFLKDPDEPPPPQPCADSLQDALLSLGSVIDV 60  
Db 1 MQAGCHSILCRSQYPAARPAEPGRQQVFLKDPDEPPPPQPCADSLQDALLSLGSVIDV 60  
QY 61 AGLOQAVKEALSAPLVKPYETVYLLDGESRLVCEPPELPHQEGKREAVISRKLGCN 120  
Db 61 AGLOQAVKEALSAPLVKPYETVYLLDGESRLVCEPPELPHQEGKREAVISRKLGCN 120  
QY 121 GLGPSDLPGKPLARLVAPLADPTQVLVPLVDKEGAVAAVILVHCGQLSDNEWSLQAV 180  
Db 121 GLGPSDLPGKPLARLVAPLADPTQVLVPLVDKEGAVAAVILVHCGQLSDNEWSLQAV 180  
QY 181 EKHTLVALKRVQALQORESSVAPEATQNPPEBAAGDQKGGVAYTQDQRKILQLCGELYDL 240  
Db 181 EKHTLVALKRVQALQORESSVAPEATQNPPEBAAGDQKGGVAYTQDQRKILQLCGELYDL 240  
QY 241 DASSLQKLVQYLOQETOASRCCLLVSDNQLQSKVIGDKVLEBEEISFPITTRGLQGV 300  
Db 241 DASSLQKLVQYLOQETOASRCCLLVSDNQLQSKVIGDKVLEBEEISFPITTRGLQGV 300  
QY 301 VEDKKSIOQLKDLTSEDQMLQSMGCEVQMLCVPISRATQVVALACAFNKLGGDLFT 360  
Db 301 VEDKKSIOQLKDLTSEDQMLQSMGCEVQMLCVPISRATQVVALACAFNKLGGDLFT 360  
QY 361 DQDEHVIQHCFTYTSVLTLSTLAFQKEQKLCCEQALLQVAKNLFTHLDDVSVLQEIIT 420  
Db 361 DQDEHVIQHCFTYTSVLTLSTLAFQKEQKLCCEQALLQVAKNLFTHLDDVSVLQEIIT 420  
QY 421 EARNLSNABICSVFLLDQNELVAKVFDGGVDESYEIRIPADQGIAGHVATTGQILNIP 480  
Db 421 EARNLSNABICSVFLLDQNELVAKVFDGGVDESYEIRIPADQGIAGHVATTGQILNIP 480

QY 481 DAYAHLFVYRGVDDSTGFRTRNLCFFPIKNEQEVIGVAELVKNKINGPWFSKFDEDLATA 540  
DB |||||  
QY 481 DAYAHLFVYRGVDDSTGFRTRNLCFFPIKNEQEVIGVAELVKNKINGPWFSKFDEDLATA 540  
DB |||||  
QY 541 FSIYCGISIAHSLLYKKVNEAQYRSHLANEMMYHMKVSDDEYTKLLHGGIQPVAADSN 600  
DB |||||  
QY 541 FSIYCGISIAHSLLYKKVNEAQYRSHLANEMMYHMKVSDDEYTKLLHGGIQPVAADSN 600  
DB |||||  
QY 601 FASFTYTPRSIPEDDTSMAILSMLQDMNFINNYKIDCPTLARFCLMWKKGVRDPPYHNWM 660  
DB |||||  
QY 601 FASFTYTPRSIPEDDTSMAILSMLQDMNFINNYKIDCPTLARFCLMWKKGVRDPPYHNWM 660  
DB |||||  
QY 661 HAFSVSHFCYLLYKNLELTNYLEDMEIPALFISCMCHDLHRGTNNSQVASKSVLAALY 720  
DB |||||  
QY 661 HAFSVSHFCYLLYKNLELTNYLEDMEIPALFISCMCHDLHRGTNNSQVASKSVLAALY 720  
DB |||||  
QY 721 SSEGSVMERHFAQAIALNTHGNCIFDHFGRKDYQRMLDLMDRIILATDLAHLRI PKD 780  
DB |||||  
QY 721 SSEGSVMERHFAQAIALNTHGNCIFDHFGRKDYQRMLDLMDRIILATDLAHLRI PKD 780  
DB |||||  
QY 781 LQKMAEVGYDRTNKQHHSLLCCLMTSCDLSQDTKGWKTTRKIAELIYKEFFSQGDLEKA 840  
DB |||||  
QY 781 LQKMAEVGYDRTNKQHHSLLCCLMTSCDLSQDTKGWKTTRKIAELIYKEFFSQGDLEKA 840  
DB |||||  
QY 841 MGNRPMEMDREKAYIPELQISFMEHIAMPYIKLLQDLFPKAAELYERVASNRHWTKVS 900  
DB |||||  
QY 841 MGNRPMEMDREKAYIPELQISFMEHIAMPYIKLLQDLFPKAAELYERVASNRHWTKVS 900  
DB |||||  
QY 901 HKFTIRGLPSNNSLDFLDEEVEVPDLOGARAPINGCCSLDAE 942  
DB |||||  
QY 901 HKFTIRGLPSNNSLDFLDEEVEVPDLOGARAPINGCCSLDAE 942  
DB |||||

## RESULT 9

PCT-US92-03222-43  
; Sequence 43, Application PC/TUS9203222  
; GENERAL INFORMATION:  
; APPLICANT: Beavo, Joseph A.  
; APPLICANT: Bentley, Kelley  
; APPLICANT: Charbonneau, Harry  
; APPLICANT: Sonnenburg, William K.  
; TITLE OF INVENTION: DNA Encoding Mammalian  
; TITLE OF INVENTION: Phosphodiesterases  
; NUMBER OF SEQUENCES: 58  
; CORRESPONDENCE ADDRESS:  
; ADDRESSEE: Marshall, O'Toole, Gerstein, Murray &  
; ADDRESSEE: Bicknell  
; STREET: Two First National Plaza, 20 South Clark  
; STREET: Street  
; CITY: Chicago  
; STATE: Illinois  
; COUNTRY: USA  
; ZIP: 60603  
; COMPUTER READABLE FORM:  
; MEDIUM TYPE: Floppy disk  
; COMPUTER: IBM PC compatible  
; OPERATING SYSTEM: PC-DOS/MS-DOS  
; SOFTWARE: Patent In Release #1.0, Version #1.25  
; CURRENT APPLICATION DATA:  
; APPLICATION NUMBER: PCT/US92/03222  
; FILING DATE: 19920420  
; CLASSIFICATION: 435  
; PRIOR APPLICATION DATA:  
; APPLICATION NUMBER: US 07/688,356  
; FILING DATE: 04-APR-1991  
; ATTORNEY/AGENT INFORMATION:  
; NAME: Noland, Greta E.  
; REGISTRATION NUMBER: 35,302  
; REFERENCE/DOCKET NUMBER: 27866/30822  
; TELECOMMUNICATION INFORMATION:  
; TELEPHONE: (312) 346-5750  
; TELEFAX: (312) 984-9740  
; TELEX: 25-3856

; INFORMATION FOR SEQ ID NO: 43:  
; SEQUENCE CHARACTERISTICS:  
; LENGTH: 942 amino acids  
; TYPE: AMINO ACID  
; TOPOLOGY: linear  
; MOLECULE TYPE: protein  
PCT-US92-03222-43

Query Match 100.0%; Score 4911; DB 5; Length 942;  
Best Local Similarity 100.0%; Pred. No. 0;  
Matches 942; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
QY 1 MGQACGSHILCRSQYPAARPAEPGRQOVFLKPEPPPPQPCADSLQDALLSLGSDIVD 60  
DB |||||  
QY 1 MGQACGSHILCRSQYPAARPAEPGRQOVFLKPEPPPPQPCADSLQDALLSLGSDIVD 60  
DB |||||  
QY 61 AGLOQAVKEALSAVLPKVETVYTYLLDGESRLVCEPPHPELPQEGKVREAVISRKLGCN 120  
DB |||||  
QY 61 AGLOQAVKEALSAVLPKVETVYTYLLDGESRLVCEPPHPELPQEGKVREAVISRKLGCN 120  
DB |||||  
QY 121 GLGPSDLPGKELARLAVAPLAPDQTVLVIPLVDKEGAAVAAILVHCGQLSNEEWSLOAV 180  
DB |||||  
QY 121 GLGPSDLPGKELARLAVAPLAPDQTVLVIPLVDKEGAAVAAILVHCGQLSNEEWSLOAV 180  
DB |||||  
QY 181 EKHTLVALKRQVALQORESSVAPEATQNPPEAAGDQKGVAYTDQDRKILQLCGELYDL 240  
DB |||||  
QY 181 EKHTLVALKRQVALQORESSVAPEATQNPPEAAGDQKGVAYTDQDRKILQLCGELYDL 240  
DB |||||  
QY 241 DASSLQLKVLQYLOQETQASRCCLLLVSEDNLQLSCKVIGDKVLEETISFPLTTGRLQGV 300  
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QY 241 DASSLQLKVLQYLOQETQASRCCLLLVSEDNLQLSCKVIGDKVLEETISFPLTTGRLQGV 300  
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QY 301 VEDKKSILQKDLTSEDMOQLQSMLGCEVOAMLCVPVISRATDQVVALACAFNKLGGDLFT 360  
DB |||||  
QY 301 VEDKKSILQKDLTSEDMOQLQSMLGCEVOAMLCVPVISRATDQVVALACAFNKLGGDLFT 360  
DB |||||  
QY 361 DQDEHVIQCHPHYTSTVLSTLAFQKEQKLCEQALLQVAKNLFTHLDDVSVLLQEIT 420  
DB |||||  
QY 361 DQDEHVIQCHPHYTSTVLSTLAFQKEQKLCEQALLQVAKNLFTHLDDVSVLLQEIT 420  
DB |||||  
QY 421 EARNLSNAEICSVFLLDQNELVAKVFDGVGVVDESYEIRIPADQGIAGHVATTGQILNIP 480  
DB |||||  
QY 421 EARNLSNAEICSVFLLDQNELVAKVFDGVGVVDESYEIRIPADQGIAGHVATTGQILNIP 480  
DB |||||  
QY 481 DAYAHLFVYRGVDDSTGFRTRNLCFFPIKNEQEVIGVAELVKNKINGPWFSKFDEDLATA 540  
DB |||||  
QY 481 DAYAHLFVYRGVDDSTGFRTRNLCFFPIKNEQEVIGVAELVKNKINGPWFSKFDEDLATA 540  
DB |||||  
QY 541 FSIYCGISIAHSLLYKKVNEAQYRSHLANEMMYHMKVSDDEYTKLLHGGIQPVAADSN 600  
DB |||||  
QY 541 FSIYCGISIAHSLLYKKVNEAQYRSHLANEMMYHMKVSDDEYTKLLHGGIQPVAADSN 600  
DB |||||  
QY 601 FASFTYTPRSIPEDDTSMAILSMLQDMNFINNYKIDCPTLARFCLMWKKGVRDPPYHNWM 660  
DB |||||  
QY 601 FASFTYTPRSIPEDDTSMAILSMLQDMNFINNYKIDCPTLARFCLMWKKGVRDPPYHNWM 660  
DB |||||  
QY 661 HAFSVSHFCYLLYKNLELTNYLEDMEIPALFISCMCHDLHRGTNNSQVASKSVLAALY 720  
DB |||||  
QY 661 HAFSVSHFCYLLYKNLELTNYLEDMEIPALFISCMCHDLHRGTNNSQVASKSVLAALY 720  
DB |||||  
QY 721 SSEGSVMERHFAQAIALNTHGNCIFDHFGRKDYQRMLDLMDRIILATDLAHLRI PKD 780  
DB |||||  
QY 721 SSEGSVMERHFAQAIALNTHGNCIFDHFGRKDYQRMLDLMDRIILATDLAHLRI PKD 780  
DB |||||  
QY 781 LQKMAEVGYDRTNKQHHSLLCCLMTSCDLSQDTKGWKTTRKIAELIYKEFFSQGDLEKA 840  
DB |||||  
QY 781 LQKMAEVGYDRTNKQHHSLLCCLMTSCDLSQDTKGWKTTRKIAELIYKEFFSQGDLEKA 840  
DB |||||  
QY 841 MGNRPMEMDREKAYIPELQISFMEHIAMPYIKLLQDLFPKAAELYERVASNRHWTKVS 900  
DB |||||  
QY 841 MGNRPMEMDREKAYIPELQISFMEHIAMPYIKLLQDLFPKAAELYERVASNRHWTKVS 900  
DB |||||  
QY 901 HKFTIRGLPSNNSLDFLDEEVEVPDLOGARAPINGCCSLDAE 942  
DB |||||

Db 901 HKFTIRGLPNSNLSDFLDEEYEVDPDGDARAPINGCCSLDAE 942

RESULT 10  
US-07-872-644-45  
; Sequence 45, Application US/07872644  
; Patent No. 5389527  
; GENERAL INFORMATION:  
; APPLICANT: Beavo, Joseph A.  
; APPLICANT: Bentley, Kelley  
; APPLICANT: Charbonneau, Harry  
; APPLICANT: Sonnenburg, William K.  
; TITLE OF INVENTION: DNA Encoding Mammalian  
; TITLE OF INVENTION: Phosphodiesterases  
; NUMBER OF SEQUENCES: 58  
; CORRESPONDENCE ADDRESS:  
; ADDRESSEE: Marshhall, O'Toole, Gerstein, Murray &  
; ADDRESS: Bicknell  
; STREET: Two First National Plaza, 20 South Clark  
; STREET: Street  
; CITY: Chicago  
; STATE: Illinois  
; COUNTRY: USA  
; ZIP: 60603  
; COMPUTER READABLE FORM:  
; MEDIUM TYPE: Floppy disk  
; OPERATING SYSTEM: PC-DOS/MS-DOS  
; SOFTWARE: Patent In Release #1.0, Version #1.25  
; CURRENT APPLICATION DATA:  
; FILING DATE: 19920420  
; CLASSIFICATION: 435  
; PRIOR APPLICATION NUMBER: US/07/872,644  
; FILING DATE: 04-APR-1991  
; ATTORNEY/AGENT INFORMATION:  
; NAME: No. 5389527and, Greta E.  
; REGISTRATION NUMBER: 35,302  
; REFERENCE/DOCKET NUMBER: 27866/30822  
; TELECOMMUNICATION INFORMATION:  
; TELEPHONE: (312) 346-5750  
; TELEFAX: (312) 984-9740  
; TELEX: 25-3856  
; INFORMATION FOR SEQ ID NO: 45:  
; SEQUENCE CHARACTERISTICS:  
; LENGTH: 941 amino acids  
; TYPE: AMINO ACID  
; TOPOLOGY: linear  
; MOLECULE TYPE: protein  
US-07-872-644-45

Query Match 96.3%; Score 4728.5; DB 1; Length 941;  
Best Local Similarity 96.0%; Pred. No. 0;  
Matches 904; Conservative 18; Mismatches 19; Indels 1; Gaps 1;  
Qy 1 MQACGHSILCSQQYPAARPAEPGRGQVFLKPDPPPPPPQPCADSLQDALLSLGSDIV 60  
Db 1 MQACGHSILCSQQYPAARPAEPGRGQVFLKPDPPPPPPQPCADSLQDALLSLGSDIV 60  
Qy 61 AGLOQAVKEALSAVLPKVTYVTVYLLDGGESRLVCEPPEPHELPQEGKREAVISRKLG 120  
Db 61 SGLQRAVKEALSAVLPKVTYVTVYLLDGGESRLVCEPPEPHELPQEGKREAVISRKLG 120  
Qy 121 GLGPSOLPGKPLARLVAFLAPDTQVLVPLVDKAGAAVAVLHVCGQLSDNEEWSLOAV 180  
Db 121 GLGPSOLPGKPLARLVAFLAPDTQVLVPLVDKAGAAVAVLHVCGQLSDNEEWSLOAV 180  
Qy 181 EKHITLVALRKVQALQORESSVAPEATONPPPEAAGDQGGVAYTDQDRKILQLCGELYDL 240  
Db 181 EKHITLVALRKVQALQORESSVAPEATONPPPEAAGDQGGVAYTDQDRKILQLCGELYDL 240

Qy 241 DASSLQLKVLQYLOQETOASRCCLLVSEDNLQLSCKVIGDKVLEBEEISFPLTTGRLGV 300  
Db 241 DASSLQLKVLQYLOQETOASRCCLLVSEDNLQLSCKVIGDKVLEBEEISFPLTTGRLGV 299  
Qy 301 VEDKKSIOQLKDLTSDMOQLOSLGCEVOAMLCVPVISRATDQVVALACAFNKLGGDLFT 360  
Db 300 VEDKKSIOQLKDLTSDMOQLOSLGCEVOAMLCVPVISRATDQVVALACAFNKLGGDLFT 359  
Qy 361 DQDEHVIQHCFTYTSVLTSTLAFQKEQKLKCECQALLQVAKNLFTHLDDVSVLQEIIT 420  
Db 360 DQDEHVIQHCFTYTSVLTSTLAFQKEQKLKCECQALLQVAKNLFTHLDDVSVLQEIIT 419  
Qy 421 EARNLSNAEICSVFLLDQNELVAKVDFGVGVDESEYIRIPADQGIAGHVAITGQILNIP 480  
Db 420 EARNLSNAEICSVFLLDQNELVAKVDFGVGVDESEYIRIPADQGIAGHVAITGQILNIP 479  
Qy 481 DAYAHLPLFYRGVDDSTGFRTRNLCFPIKNEQNEQVIGVAELVNKINGPMWFSKFDLATA 540  
Db 480 DAYAHLPLFYRGVDDSTGFRTRNLCFPIKNEQNEQVIGVAELVNKINGPMWFSKFDLATA 539  
Qy 541 FSIYCGISIAHSLLYKKNVNEAQYRSHLANEMMYHMKVSDDEYTKLLHDGIQPVAAIDSN 600  
Db 540 FSIYCGISIAHSLLYKKNVNEAQYRSHLANEMMYHMKVSDDEYTKLLHDGIQPVAAIDSN 599  
Qy 601 FASFTYTPRSLPDDTSMALLSMLQDMNFINNYKIDCPTLARFCLMVKGYRDPYPHNMM 660  
Db 600 FASFTYTPRSLPDDTSMALLSMLQDMNFINNYKIDCPTLARFCLMVKGYRDPYPHNMM 659  
Qy 661 HAFVSVSHFCYLLYKNLEUTNYLEDMEIFALFTSCMCHDLDRGTNNNSFOVASKSVLAALY 720  
Db 660 HAFVSVSHFCYLLYKNLEUTNYLEDMEIFALFTSCMCHDLDRGTNNNSFOVASKSVLAALY 719  
Qy 721 SSEGSMERHFAQAIAILNTHGNCNIPDFSRKQYQRMLDLMDRIILATDLAHLRIKPD 780  
Db 720 SSEGSMERHFAQAIAILNTHGNCNIPDFSRKQYQRMLDLMDRIILATDLAHLRIKPD 779  
Qy 781 LQKMAEVGYDRTNKQHHSLILCLMTSCDLSQDTQGWKTRKIAELIYKEPFSQGDLEKA 840  
Db 780 LQKMAEVGYDRTNKQHHSLILCLMTSCDLSQDTQGWKTRKIAELIYKEPFSQGDLEKA 839  
Qy 841 MGNRPMEWMREKAYIPELOISFMEHIAPIYKLLQDLFPKAAELYERVASNREHWTKVS 900  
Db 840 MGNRPMEWMREKAYIPELOISFMEHIAPIYKLLQDLFPKAAELYERVASNREHWTKVS 899  
Qy 901 HKFTIRGLPNSNLSDFLDEEYEVDPDGDARAPINGCCSLDAE 942  
Db 900 HKFTIRGLPNSNLSDFLDEEYEVDPDGDARAPINGCCSLDAE 941

RESULT 11  
US-08-297-494-45  
; Sequence 45, Application US/08297494  
; Patent No. 5580771  
; GENERAL INFORMATION:  
; APPLICANT: Beavo, Joseph A.  
; APPLICANT: Bentley, Kelley  
; APPLICANT: Charbonneau, Harry  
; APPLICANT: Sonnenburg, William K.  
; TITLE OF INVENTION: DNA Encoding Mammalian  
; TITLE OF INVENTION: Phosphodiesterases  
; NUMBER OF SEQUENCES: 58  
; CORRESPONDENCE ADDRESS:  
; ADDRESSEE: Marshhall, O'Toole, Gerstein, Murray &  
; ADDRESS: Bicknell  
; STREET: Two First National Plaza, 20 South Clark  
; STREET: Street  
; CITY: Chicago  
; STATE: Illinois  
; COUNTRY: USA  
; ZIP: 60603  
; COMPUTER READABLE FORM:  
; MEDIUM TYPE: Floppy disk  
; COMPUTER: IBM PC compatible

OPERATING SYSTEM: PC-DOS/MS-DOS  
SOFTWARE: PatentIn Release #1.0, Version #1.25  
CURRENT APPLICATION DATA: US/08/297,494  
FILING DATE:  
CLASSIFICATION: 435  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: US 07/688,356  
FILING DATE: 04-APR-1991  
ATTORNEY/AGENT INFORMATION:  
NAME: No. 558077land, Greta E.  
REGISTRATION NUMBER: 35,302  
REFERENCE/DOCKET NUMBER: 27866/30822  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: (312) 346-5750  
TELEFAX: (312) 984-9740  
TELEX: 25-3856  
INFORMATION FOR SEQ ID NO: 45:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 941 amino acids  
TYPE: amino acid  
TOPOLOGY: linear  
MOLECULE TYPE: protein  
US-08-297-494-45

Query Match 96.3%; Score 4728.5; DB 1; Length 941;  
Best Local Similarity 96.0%; Pred. No. 0;  
Matches 904; Conservative 18; Mismatches 19; Indels 1; Gaps 1;  
  
Qy 1 MQACGHSILCSQOYPAARPAERGGQVFLKPEPPPPPPPCADSLQDALLSLGSDIVD 60  
Db 1 MQACGHSILCSQOYPAARPAERGGQVFLKPEPPPPPPPCADSLQDALLSLGSDIVD 60  
  
Qy 61 AGLOAVKEALSAPLKVETVYVYLLDGSRLVCEPPHLPQEGKREAVISKRIGCN 120  
Db 61 SGLQRAVKEALSAPLKVETVYVYLLDGSRLVCEPPHLPQEGKREAVISKRIGCN 120  
  
Qy 121 GLGPSDLPGKPLARLVAFLADPTQVLPVYDKAGAAVAVILVHCGQLSDNEWSLOAV 180  
Db 121 GLGPSDLPGKPLARLVAFLADPTQVLPVYDKAGAAVAVILVHCGQLSDNEWSLOAV 180  
  
Qy 181 EKHTLVALKRVQALQORESSVAPATONPPPEAAGDQKGVAYTDQDKILQLCGELYDL 240  
Db 181 EKHTLVALKRVQALQORESSVAPATONPPPEAAGDQKGVAYTDQDKILQLCGELYDL 240  
  
Qy 241 DASSLQLKVLQYLOQETOASRCCLLLVSEDNLQLSCKVIGDKVLEELISFPLTTGRIGQV 300  
Db 241 DASSLQLKVLQYLOQETOASRCCLLLVSEDNLQLSCKVIGDKVLEELISFPLTTGRIGQV 300  
  
Qy 301 VEDKKSIOQLKDLTSEDMOQLSMLGCEVOAMLCVPVISRATDOVVVALACAFNKLGGDLFT 360  
Db 300 VEDKKSIOQLKDLTSEDVQOQLSMLGCELOAMLCVPVISRATDOVVVALACAFNKLGGDLFT 359  
  
Qy 361 DODEHVIQCHFYTSVLTSTLAFQEKQKCECOALLQVAKNLFTHLDDVSVLLQEIIT 420  
Db 360 DODEHVIQCHFYTSVLTSTLAFQEKQKCECOALLQVAKNLFTHLDDVSVLLQEIIT 419  
  
Qy 421 EARLNSNAEISCVFLDDQNELVAKVFDGGVVEDESEYIRIPADQGIAGHVATTGQILNIP 480  
Db 420 EARLNSNAEISCVFLDDQNELVAKVFDGGVVEDESEYIRIPADQGIAGHVATTGQILNIP 479  
  
Qy 481 DAYAHLPIYRGVDDSTGFRTRNLCFPPIKNENQEVIGVAELVNKINGPWFSKFDEDLATA 540  
Db 480 DAYAHLPIYRGVDDSTGFRTRNLCFPPIKNENQEVIGVAELVNKINGPWFSKFDEDLATA 539  
  
Qy 541 FSIYCGISIAHSLYKKYNEAQYRSHLANEMMHKVSDDDEYTKLLHDGQIPVAADSN 600  
Db 540 FSIYCGISIAHSLYKKYNEAQYRSHLANEMMHKVSDDDEYTKLLHDGQIPVAADSN 599  
  
Qy 601 FASFTYTPRSLPEDDTSMAILSMLODMNFNNYKIDCPTLARFCMLVKGYRDPYPYNNWM 660  
Db 600 FASFTYTPRSLPEDDTSMAILSMLODMNFNNYKIDCPTLARFCMLVKGYRDPYPYNNWM 659

Qy 661 HAPSVSHFCVLLYKNLELTNLYLDEMEIFALFISCMCHDLDRGTNNNSFOVASKSVLAALY 720  
Db 660 HAPSVSHFCVLLYKNLELTNLYLDEMEIFALFISCMCHDLDRGTNNNSFOVASKSVLAALY 719  
  
Qy 721 SSEGSMERHHFAQAIAILNTHGNCNIFDHFSSKDYQRMQLDMRDIIILATDLAHLRIFKD 780  
Db 720 SSEGSMERHHFAQAIAILNTHGNCNIFDHFSSKDYQRMQLDMRDIIILATDLAHLRIFKD 779  
  
Qy 781 LQKMAEYGYDRTNKQHSLLCLLMTSCDLSQDTKGWKTTRKIAELIYKEFPFSGDLEKA 840  
Db 780 LQKMAEYGYDRTNKQHSLLCLLMTSCDLSQDTKGWKTTRKIAELIYKEFPFSGDLEKA 839  
  
Qy 841 MGNRPMBMDREKAYIPELQISFMEHTAMPTIKLQDLFPKAAELYERVASNRHHTWKVS 900  
Db 840 MGNRPMBMDREKAYIPELQISFMEHTAMPTIKLQDLFPKAAELYERVASNRHHTWKVS 899  
  
Qy 901 HKFTIRGLPSNNSLDLDEEYVDPDLGAPINGCCSLDAE 942  
Db 900 HKFTIRGLPSNNSLDLDEEYVDPDLGAPINGCCSLDAE 941

RESULT 12  
US-08-297-510-45  
Sequence 45, Application US/08297510  
Patent No. 5602019  
GENERAL INFORMATION:  
APPLICANT: Beavo, Joseph A.  
APPLICANT: Bentley, Kelley  
APPLICANT: Charbonneau, Harry  
APPLICANT: Sonnenburg, William K.  
TITLE OF INVENTION: DNA Encoding Mammalian  
TITLE OF INVENTION: Phosphodiesterases  
NUMBER OF SEQUENCES: 58  
CORRESPONDENCE ADDRESS:  
ADDRESSEE: Marshall, O'Toole, Gerstein, Murray &  
ADDRESSEE: Bicknell  
STREET: Two First National Plaza, 20 South Clark  
CITY: Chicago  
STATE: Illinois  
COUNTRY: USA  
ZIP: 60603  
COMPUTER READABLE FORM:  
MEDIUM TYPE: Floppy disk  
COMPUTER: IBM PC compatible  
OPERATING SYSTEM: PC-DOS/MS-DOS  
SOFTWARE: PatentIn Release #1.0, Version #1.25  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/08/297,510  
FILING DATE:  
CLASSIFICATION: 435  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: US 07/688,356  
FILING DATE: 04-APR-1991  
ATTORNEY/AGENT INFORMATION:  
NAME: No. 5602019and, Greta E.  
REGISTRATION NUMBER: 35,302  
REFERENCE/DOCKET NUMBER: 27866/30822  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: (312) 346-5750  
TELEFAX: (312) 984-9740  
TELEX: 25-3856  
INFORMATION FOR SEQ ID NO: 45:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 941 amino acids  
TYPE: amino acid  
TOPOLOGY: linear  
MOLECULE TYPE: protein  
US-08-297-510-45

Query Match 96.3%; Score 4728.5; DB 1; Length 941;  
Best Local Similarity 96.0%; Pred. No. 0;  
Matches 904; Conservative 18; Mismatches 19; Indels 1; Gaps 1;



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QY 1 MGQACGHSILCRSQYPAARPAEPRGQQVFLKDPDEPPPPPPQPCADSLQDALLSLGSDIV 60
Db 1 MGQACGHSILCRSQYPAARPAEPRGQQVFLKDPDEPPPPPPQPCADSLQDALLSLGSDIV 60
QY 61 AGLOQAVKEALSAVLPKVTYVTVLLDGSRLVCEPPELPOEGKVRVAVTSRKLGCN 120
Db 61 SGLQRAVKALSAVLPKVTYVTVLLDGSRLVCEPPELPOEGKVRVAVTSRKLGCN 120
QY 121 GLGPSDLPGKPLARLVAFLAPDQVLPVPLVDKEAGAAVAVILVHCQSLSDNEEWSLQAV 180
Db 121 GLGPSDLPGKPLARLVAFLAPDQVLPVPLVDKEAGAAVAVILVHCQSLSDNEEWSLQAV 180
QY 181 EKHTLVALKRVQALQORESSVAPEATONPPESAAGQKGGVAYTDDRKILQCGELYDL 240
Db 181 EKHTLVALKRVQALQORESSVAPEATONPPESAAGQKGGVAYTDDRKILQCGELYDL 240
QY 241 DASSLQKLVQYLOQRTASRCCLLVSDNLQSLCKVIGDKVLEIEISFPLTTGRLGV 300
Db 241 DASSLQKLVQYLOQRTASRCCLLVSDNLQSLCKVIGDKVLEIEISFPLTTGRLGV 300
QY 301 VEDKKSIOQLKDLTSDVQQLQSLMGCLEQAMLCVPVISRATQVVALACAFNKLGGDLFT 360
Db 301 VEDKKSIOQLKDLTSDVQQLQSLMGCLEQAMLCVPVISRATQVVALACAFNKLGGDLFT 360
QY 360 DEDEHVIQCHFYHTSVLTSTLAFQEKQKCEQALLQVAKNLFTHLDDVSVLLQEIT 419
Db 360 DEDEHVIQCHFYHTSVLTSTLAFQEKQKCEQALLQVAKNLFTHLDDVSVLLQEIT 419
QY 421 EARNLSNABICSVFLDQNELVAKVFDGGVDESEYIEIRIPADQGIAGHVAATGQILNP 480
Db 421 EARNLSNABICSVFLDQNELVAKVFDGGVDESEYIEIRIPADQGIAGHVAATGQILNP 480
QY 480 DAYAHLPLFRGVDDSTGFRTRILCPPIKNEQVIGVLAELVKNKINGPWFSDDEDLATA 539
Db 480 DAYAHLPLFRGVDDSTGFRTRILCPPIKNEQVIGVLAELVKNKINGPWFSDDEDLATA 539
QY 541 FSIYCGISIAHLLYKKNVNAQVRSRLANEMMYHMKVSDDEYTKLLHDGIIQFVAIDSN 600
Db 541 FSIYCGISIAHLLYKKNVNAQVRSRLANEMMYHMKVSDDEYTKLLHDGIIQFVAIDSN 600
QY 601 FASFTYTPRSLPDDTSMALSLQDMFNINNYKIDCPTLAFCLMVKKGYRDPYHNM 660
Db 601 FASFTYTPRSLPDDTSMALSLQDMFNINNYKIDCPTLAFCLMVKKGYRDPYHNM 660
QY 661 HAFVSVSHFCVLYKXLELNYLEDMEIFALFISCMCHDLDRGTNNISFOVASKSVLAALY 720
Db 661 HAFVSVSHFCVLYKXLELNYLEDMEIFALFISCMCHDLDRGTNNISFOVASKSVLAALY 720
QY 721 SSEGVSMEHRHFAQAIATLNTGHCNIFDHSRKYQRMVLDLMDRIILATDLAHLRIKPD 780
Db 721 SSEGVSMEHRHFAQAIATLNTGHCNIFDHSRKYQRMVLDLMDRIILATDLAHLRIKPD 780
QY 781 LQKMAEVGDRNKKHSHLLCLLMTSCDLSQDTGKWKTRKIAELIYKEFFSQGDLEKA 840
Db 781 LQKMAEVGDRNKKHSHLLCLLMTSCDLSQDTGKWKTRKIAELIYKEFFSQGDLEKA 840
QY 841 MGNRPMEWMMDREKAVIPELQISFMHEIAMPYIKLQDLFPKAELEYERVASNRHWTKVS 900
Db 841 MGNRPMEWMMDREKAVIPELQISFMHEIAMPYIKLQDLFPKAELEYERVASNRHWTKVS 900
QY 901 HKFTIRGLPSNNSLDFDEYEVPLDGCARAPINGCCSLDAE 942
Db 901 HKFTIRGLPSNNSLDFDEYEVPLDGCARAPINGCCSLDAE 942
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## RESULT 13

US-08-479-532-45  
; Sequence 45, Application US/08479532  
; Patent No. 5776752  
; GENERAL INFORMATION:  
; APPLICANT: Beavo, Joseph A.  
; APPLICANT: Bentley, Kelley

APPLICANT: Charbonneau, Harry  
APPLICANT: Sonnenburg, William K.  
TITLE OF INVENTION: DNA Encoding Mammalian  
TITLE OF INVENTION: Phosphodiesterases  
NUMBER OF SEQUENCES: 58  
CORRESPONDENCE ADDRESS:  
ADDRESSES: Marshhall, O'Toole, Gerstein, Murray &  
ADDRESSES: Bicknell  
STREET: Two First National Plaza, 20 South Clark  
STREET: Street  
CITY: Chicago  
STATE: Illinois  
COUNTRY: USA  
ZIP: 60603  
COMPUTER READABLE FORM:  
MEDIUM TYPE: Floppy disk  
COMPUTER: IBM PC compatible  
OPERATING SYSTEM: PC-DOS/MS-DOS  
SOFTWARE: Patent In Release #1.0, Version #1.25  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/08/479,532  
FILING DATE: 07-JUN-1995  
CLASSIFICATION: 435  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: 08/297,494  
FILING DATE:  
APPLICATION NUMBER: US 07/688,356  
FILING DATE: 04-APR-1991  
ATTORNEY/AGENT INFORMATION:  
NAME: No. 5776752and, Greta E.  
REGISTRATION NUMBER: 35,302  
REFERENCE/DOCKET NUMBER: 27866/30822  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: (312) 346-5750  
TELEFAX: (312) 984-9740  
TELEX: 25-3856  
INFORMATION FOR SEQ ID NO: 45:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 941 amino acids  
TYPE: amino acid  
TOPOLOGY: linear  
MOLESCULE TYPE: protein  
US-08-479-532-45

Query Match 96.3%; Score 4728.5; DB 1; Length 941;

Best Local Similarity 96.0%; Pred. No. 0;

Matches 904; Conservative 18; Mismatches 19; Indels 1; Gaps 1;

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QY 1 MGQACGHSILCRSQYPAARPAEPRGQQVFLKDPDEPPPPPPQPCADSLQDALLSLGSDIV 60
Db 1 MGQACGHSILCRSQYPAARPAEPRGQQVFLKDPDEPPPPPPQPCADSLQDALLSLGSDIV 60
QY 61 AGLOQAVKEALSAVLPKVTYVTVLLDGSRLVCEPPELPOEGKVRVAVTSRKLGCN 120
Db 61 SGLQRAVKALSAVLPKVTYVTVLLDGSRLVCEPPELPOEGKVRVAVTSRKLGCN 120
QY 121 GLGPSDLPGKPLARLVAFLAPDQVLPVPLVDKEAGAAVAVILVHCQSLSDNEEWSLQAV 180
Db 121 GLGPSDLPGKPLARLVAFLAPDQVLPVPLVDKEAGAAVAVILVHCQSLSDNEEWSLQAV 180
QY 181 EKHTLVALKRVQALQORESSVAPEATONPPESAAGQKGGVAYTDDRKILQCGELYDL 240
Db 181 EKHTLVALKRVQALQORESSVAPEATONPPESAAGQKGGVAYTDDRKILQCGELYDL 240
QY 241 DASSLQKLVQYLOQRTASRCCLLVSDNLQSLCKVIGDKVLEIEISFPLTTGRLGV 300
Db 241 DASSLQKLVQYLOQRTASRCCLLVSDNLQSLCKVIGDKVLEIEISFPLTTGRLGV 300
QY 301 VEDKKSIOQLKDLTSDVQQLQSLMGCLEQAMLCVPVISRATQVVALACAFNKLGGDLFT 360
Db 301 VEDKKSIOQLKDLTSDVQQLQSLMGCLEQAMLCVPVISRATQVVALACAFNKLGGDLFT 360
QY 360 DEDEHVIQCHFYHTSVLTSTLAFQEKQKCEQALLQVAKNLFTHLDDVSVLLQEIT 420
Db 360 DEDEHVIQCHFYHTSVLTSTLAFQEKQKCEQALLQVAKNLFTHLDDVSVLLQEIT 420
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;
; APPLICATION NUMBER: US 07/688,356
; FILING DATE: 04-APR-1991
; ATTORNEY/AGENT INFORMATION:
; NAME: No. 578953and, Greta E.
; REGISTRATION NUMBER: 35,302
; REFERENCE/DOCKET NUMBER: 27866/30822
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (312) 346-5750
; TELEFAX: (312) 984-9740
; TELEX: 25-3856
; INFORMATION FOR SEQ ID NO: 45:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 941 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: protein
US-08-455-526-45

Query Match          96.3%; Score 4728.5; DB 1; Length 941;
Best Local Similarity 96.0%; Pred. No. 0;
Matches 904; Conservative 18; Mismatches 19; Indels 1; Gaps 1;

QY 1 MGQACGSHILCRSQYPAARPAEPRGQGVFLKPDPEPPPPQPCADSLQDALLSLGSDIV 60
DB 1 MGQACGSHILCRSQYPAARPAEPRGQGVFLKPDPEPPPPQPCADSLQDALLSLGSDIV 60

QY 61 AGLOQAVKEALSAVLPKVETVYTYLLDGSRLVCEBPHELPOEGKVREAVISRKLGCN 120
DB 61 SGLQAVKEALSAVLPKVETVYTYLLDGSRLVCEBPHELPOEGKVREAVISRKLGCN 120

QY 121 GLGSDLPGLPRLARLAPLAPDQVLPVLDKAGAAVAAILVHCGQLSNEEWSLOAV 180
DB 121 GLGSDLPGLPRLARLAPLAPDQVLPVLDKAGAAVAAILVHCGQLSNEEWSLOAV 180

QY 181 EKHTLVALKRVALQORESSVAPEATQNPPEAAAGQKGVAYTDQDRKILQLCGELYDL 240
DB 181 EKHTLVALKRVALQORESSVAPEATQNPPEAAAGQKGVAYTDQDRKILQLCGELYDL 240

QY 241 DASSLQLKVLQYLOQETQASRCCLLLYSEDNLQLSCKVIGDKVLEESPLTTGRLGOV 300
DB 241 DASSLQLKVLQYLOQETQASRCCLLLYSEDNLQLSCKVIGDKVLEESPLTTGRLGOV 300

QY 301 VEDKKSITQLKDLTSEDMDQQLQSMGLCEVQAMLCVPVISRATDQVVALACAFNKLGDLFT 360
DB 301 VEDKKSITQLKDLTSEDMDQQLQSMGLCEVQAMLCVPVISRATDQVVALACAFNKLGDLFT 360

QY 361 DQDEHVIQCHPHYTSTVLSTLAFQKQKLCCECOALLQVAKNLFTHLDDVSVLLQEIT 420
DB 361 DQDEHVIQCHPHYTSTVLSTLAFQKQKLCCECOALLQVAKNLFTHLDDVSVLLQEIT 420

QY 421 EARNLSNAEITCSVFLLDQNELVAKVFDGQVVEDESYEIRIPADQGIAGHVATTGQILNIP 480
DB 421 EARNLSNAEITCSVFLLDQNELVAKVFDGQVVEDESYEIRIPADQGIAGHVATTGQILNIP 480

QY 481 DAYAHLPLFYRGVDDSTGFRTRNLCFPIKNEQVIGVAELVNKINGPWFSKFDEDLATA 540
DB 481 DAYAHLPLFYRGVDDSTGFRTRNLCFPIKNEQVIGVAELVNKINGPWFSKFDEDLATA 540

QY 541 FSIYCGISIAHSLLYKKVNEAQYRSHLANEMMYHMKVSDDEYTKLLHDGQIPVAAIDSN 600
DB 541 FSIYCGISIAHSLLYKKVNEAQYRSHLANEMMYHMKVSDDEYTKLLHDGQIPVAAIDSN 600

QY 601 FASFTYTPRSLPEDDTSMAILSMLQDMNFINNYKIDCPTLARFCIMVKKGVRDPPYHNWM 660
DB 601 FASFTYTPRSLPEDDTSMAILSMLQDMNFINNYKIDCPTLARFCIMVKKGVRDPPYHNWM 660

QY 661 HAFSVSHFCYLLYKNLELTNYLEDMEIFALFISCMCHDLHRGTNNNSFQVASKSVLAALY 720
DB 661 HAFSVSHFCYLLYKNLELTNYLEDMEIFALFISCMCHDLHRGTNNNSFQVASKSVLAALY 720

QY 721 SSEGSMERHHFAQAIAILNTHGNCNIFDHFSRKDYQRMLDLMDRIILATDLAHLRIPKD 780
DB 721 SSEGSMERHHFAQAIAILNTHGNCNIFDHFSRKDYQRMLDLMDRIILATDLAHLRIPKD 780

QY 781 LQKMAEVGYDRNKKQHSLLCLLMTSCDLSQTKGWKTKRIABLIYKPFPSQGDLEKA 840
DB 781 LQKMAEVGYDRNKKQHSLLCLLMTSCDLSQTKGWKTKRIABLIYKPFPSQGDLEKA 840

QY 841 MGNRMENMMDREKAVIPELOISFMEHIAWPIYKLLQDLFPKAAELYERVAASRHHWTKVS 900
DB 841 MGNRMENMMDREKAVIPELOISFMEHIAWPIYKLLQDLFPKAAELYERVAASRHHWTKVS 900

QY 901 HKFTIRGLPNSNSLDLFDDEYEVPLDGCARAPINGCCSLDAE 942
DB 901 HKFTIRGLPNSNSLDLFDDEYEVPLDGCARAPINGCCSLDAE 942

;
; RESULT 14
; US-08-455-526-45
; Sequence 45, Application US/08455526
; Patent No. 5789553
; GENERAL INFORMATION:
; APPLICANT: Beavo, Joseph A.
; APPLICANT: Bentley, Kelley
; APPLICANT: Charbonneau, Harry
; APPLICANT: Sonnenburg, William K.
; TITLE OF INVENTION: DNA Encoding Mammalian
; TITLE OF INVENTION: Phosphodiesterases
; NUMBER OF SEQUENCES: 58
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Marshall, O'Toole, Gerstein, Murray &
; ADDRESSEE: Bicknell
; STREET: Two First National Plaza, 20 South Clark
; STREET: Street
; CITY: Chicago
; STATE: Illinois
; COUNTRY: USA
; ZIP: 60603
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patent In Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/455,526
; FILING DATE: 31-MAY-1995
; CLASSIFICATION: 530
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/297,494
; FILING DATE: 29-AUG-1994

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;
; APPLICATION NUMBER: US 07/688,356
; FILING DATE: 04-APR-1991
; ATTORNEY/AGENT INFORMATION:
; NAME: No. 578953and, Greta E.
; REGISTRATION NUMBER: 35,302
; REFERENCE/DOCKET NUMBER: 27866/30822
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (312) 346-5750
; TELEFAX: (312) 984-9740
; TELEX: 25-3856
; INFORMATION FOR SEQ ID NO: 45:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 941 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: protein
US-08-455-526-45

Query Match          96.3%; Score 4728.5; DB 1; Length 941;
Best Local Similarity 96.0%; Pred. No. 0;
Matches 904; Conservative 18; Mismatches 19; Indels 1; Gaps 1;

QY 1 MGQACGSHILCRSQYPAARPAEPRGQGVFLKPDPEPPPPQPCADSLQDALLSLGSDIV 60
DB 1 MGQACGSHILCRSQYPAARPAEPRGQGVFLKPDPEPPPPQPCADSLQDALLSLGSDIV 60

QY 61 AGLOQAVKEALSAVLPKVETVYTYLLDGSRLVCEBPHELPOEGKVREAVISRKLGCN 120
DB 61 SGLQAVKEALSAVLPKVETVYTYLLDGSRLVCEBPHELPOEGKVREAVISRKLGCN 120

QY 121 GLGSDLPGLPRLARLAPLAPDQVLPVLDKAGAAVAAILVHCGQLSNEEWSLOAV 180
DB 121 GLGSDLPGLPRLARLAPLAPDQVLPVLDKAGAAVAAILVHCGQLSNEEWSLOAV 180

QY 181 EKHTLVALKRVALQORESSVAPEATQNPPEAAAGQKGVAYTDQDRKILQLCGELYDL 240
DB 181 EKHTLVALKRVALQORESSVAPEATQNPPEAAAGQKGVAYTDQDRKILQLCGELYDL 240

QY 241 DASSLQLKVLQYLOQETQASRCCLLLYSEDNLQLSCKVIGDKVLEESPLTTGRLGOV 300
DB 241 DASSLQLKVLQYLOQETQASRCCLLLYSEDNLQLSCKVIGDKVLEESPLTTGRLGOV 300

QY 301 VEDKKSITQLKDLTSEDMDQQLQSMGLCEVQAMLCVPVISRATDQVVALACAFNKLGDLFT 360
DB 301 VEDKKSITQLKDLTSEDMDQQLQSMGLCEVQAMLCVPVISRATDQVVALACAFNKLGDLFT 360

QY 361 DQDEHVIQCHPHYTSTVLSTLAFQKQKLCCECOALLQVAKNLFTHLDDVSVLLQEIT 420
DB 361 DQDEHVIQCHPHYTSTVLSTLAFQKQKLCCECOALLQVAKNLFTHLDDVSVLLQEIT 420

QY 421 EARNLSNAEITCSVFLLDQNELVAKVFDGQVVEDESYEIRIPADQGIAGHVATTGQILNIP 480
DB 421 EARNLSNAEITCSVFLLDQNELVAKVFDGQVVEDESYEIRIPADQGIAGHVATTGQILNIP 480

QY 481 DAYAHLPLFYRGVDDSTGFRTRNLCFPIKNEQVIGVAELVNKINGPWFSKFDEDLATA 540
DB 481 DAYAHLPLFYRGVDDSTGFRTRNLCFPIKNEQVIGVAELVNKINGPWFSKFDEDLATA 540

QY 541 FSIYCGISIAHSLLYKKVNEAQYRSHLANEMMYHMKVSDDEYTKLLHDGQIPVAAIDSN 600
DB 541 FSIYCGISIAHSLLYKKVNEAQYRSHLANEMMYHMKVSDDEYTKLLHDGQIPVAAIDSN 600

QY 601 FASFTYTPRSLPEDDTSMAILSMLQDMNFINNYKIDCPTLARFCIMVKKGVRDPPYHNWM 660
DB 601 FASFTYTPRSLPEDDTSMAILSMLQDMNFINNYKIDCPTLARFCIMVKKGVRDPPYHNWM 660

QY 661 HAFSVSHFCYLLYKNLELTNYLEDMEIFALFISCMCHDLHRGTNNNSFQVASKSVLAALY 720
DB 661 HAFSVSHFCYLLYKNLELTNYLEDMEIFALFISCMCHDLHRGTNNNSFQVASKSVLAALY 720

QY 721 SSEGSMERHHFAQAIAILNTHGNCNIFDHFSRKDYQRMLDLMDRIILATDLAHLRIPKD 780
DB 721 SSEGSMERHHFAQAIAILNTHGNCNIFDHFSRKDYQRMLDLMDRIILATDLAHLRIPKD 780

QY 781 LQKMAEVGYDRNKKQHSLLCLLMTSCDLSQTKGWKTKRIABLIYKPFPSQGDLEKA 840
DB 781 LQKMAEVGYDRNKKQHSLLCLLMTSCDLSQTKGWKTKRIABLIYKPFPSQGDLEKA 840

QY 841 MGNRMENMMDREKAVIPELOISFMEHIAWPIYKLLQDLFPKAAELYERVAASRHHWTKVS 900
DB 841 MGNRMENMMDREKAVIPELOISFMEHIAWPIYKLLQDLFPKAAELYERVAASRHHWTKVS 900

QY 901 HKFTIRGLPNSNSLDLFDDEYEVPLDGCARAPINGCCSLDAE 942
DB 901 HKFTIRGLPNSNSLDLFDDEYEVPLDGCARAPINGCCSLDAE 942

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[illegible]

RESULT 15

US-08-455-525-45  
; Sequence 45, Application US/08455525  
; Patent No. 5800987  
; GENERAL INFORMATION:  
; APPLICANT: Beavo, Joseph A.  
; APPLICANT: Bentley, Kelley  
; APPLICANT: Charbonneau, Harry  
; APPLICANT: Sonnenbom, William K.  
; TITLE OF INVENTION: DNA Encoding Mammalian  
; TITLE OF INVENTION: Phosphodiesterases  
; NUMBER OF SEQUENCES: 58  
; CORRESPONDENCE ADDRESS:  
; ADDRESSEE: Marshall, O'Toole, Gerstein, Murray &  
; ADDRESSEE: Bicknell  
; STREET: Two First National Plaza, 20 South Clark  
; STREET: Street  
; CITY: Chicago  
; STATE: Illinois  
; COUNTRY: USA  
; ZIP: 60603  
; COMPUTER READABLE FORM:  
; MEDIUM TYPE: Floppy disk  
; COMPUTER: IBM PC compatible  
; OPERATING SYSTEM: PC-DOS/MS-DOS  
; SOFTWARE: Patent In Release #1.0, Version #1.25  
; CURRENT APPLICATION DATA:  
; APPLICATION NUMBER: US/08/455,525  
; FILING DATE: 31-MAY-1995  
; CLASSIFICATION: 435  
; PRIORITY APPLICATION DATA:  
; APPLICATION NUMBER: 08/297,494  
; FILING DATE:  
; APPLICATION NUMBER: US 07/688,356  
; FILING DATE: 04-APR-1991  
; ATTORNEY/AGENT INFORMATION:  
; NAME: No. 5800987and, Greta E.  
; REGISTRATION NUMBER: 35,302  
; REFERENCE/DOCKET NUMBER: 27866/30822  
; TELECOMMUNICATION INFORMATION:  
; TELEPHONE: (312) 346-5750  
; TELEFAX: (312) 984-9740  
; TELEX: 25-3856  
; INFORMATION FOR SEQ ID NO: 45:  
; SEQUENCE CHARACTERISTICS:  
; LENGTH: 941 amino acids  
; TYPE: amino acid  
; TOPOLOGY: linear  
; MOLECULE TYPE: protein  
US-08-455-525-45

Query Match 96.3%; Score 4728.5; DB 1; Length 941;  
Best Local Similarity 96.0%; Pred. No. 0;  
Matches 904; Conservative 18; Mismatches 19; Indels 1; Gaps 1

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[illegible]

Search completed: June 26, 2005, 12:24:06  
Job time : 34.8438 secs

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GenCore version 5.1.6  
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OM protein - protein search, using sw model

Run on: June 26, 2005, 12:21:57 ; Search time 117.308 Seconds  
(without alignments)  
3087.987 Million cell updates/sec

Title: US-10-697-894-43  
Perfect score: 4911  
Sequence: 1 MQACCHSILCRSQYPAAR.....VPLDGLARAPINGCCSLDAE 942

Scoring table: BLOSUM62  
Gapop 10.0 , Gapext 0.5

Searched: 1717557 seqs, 384547976 residues

Total number of hits satisfying chosen parameters: 1717557

Minimum DB seq length: 0  
Maximum DB seq length: 2000000000  
Post-processing: Minimum Match 0%  
Maximum Match 100%  
Listing first 45 summaries

Database : Published Applications AA:\*  
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22: /cgn2\_6/ptodata/2/pubpaa/US60\_PUBCOMB.pep.\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

#### SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	4911	100.0	942	9	US-09-883-825-43
2	4911	100.0	942	16	US-10-697-894-43
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4	4728.5	96.3	941	16	US-10-697-894-45
5	4728.5	96.3	941	16	US-10-686-390-5
6	4728.5	96.3	941	17	US-10-686-282-5
7	4728.5	96.3	941	17	US-10-686-349-5
8	4657	94.8	921	9	US-09-883-825-39
9	4657	94.8	921	13	US-10-094-989-5
10	4657	94.8	921	16	US-10-697-894-39
11	4530.5	92.3	905	13	US-10-094-989-4
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					Sequence 43, Appl
					Sequence 45, Appl
					Sequence 45, Appl
					Sequence 5, Appl
					Sequence 5, Appl
					Sequence 5, Appl
					Sequence 39, Appl
					Sequence 5, Appl
					Sequence 39, Appl
					Sequence 4, Appl

12 4480.5 91.2 920 15 US-10-236-417-78 Sequence 78, Appl  
13 4474.5 91.1 920 13 US-10-094-989-2 Sequence 2, Appl  
14 4272.5 87.0 950 15 US-10-108-260A-2928 Sequence 2928, Ap  
15 3484.5 71.0 786 15 US-10-104-047-2944 Sequence 2944, Ap  
16 1766 36.0 334 17 US-10-771-833-30 Sequence 30, Appl  
17 1766 36.0 334 17 US-10-886-949-30 Sequence 30, Appl  
18 586 20.1 934 9 US-09-891-216-12 Sequence 12, Appl  
19 586 20.1 934 9 US-09-891-216-12 Sequence 12, Appl  
20 586 20.1 934 14 US-10-168-402-2 Sequence 5, Appl  
21 586 20.1 934 14 US-10-168-402-2 Sequence 5, Appl  
22 969.5 19.7 934 14 US-10-168-402-39 Sequence 39, Appl  
23 920.5 18.7 684 9 US-09-891-216-14 Sequence 14, Appl  
24 920.5 18.7 684 14 US-10-168-402-4 Sequence 4, Appl  
25 920.5 18.7 684 16 US-10-746-197-1 Sequence 1, Appl  
26 913.5 18.6 779 9 US-09-420-190-1 Sequence 1, Appl  
27 913.5 18.6 779 15 US-10-458-839-1 Sequence 1, Appl  
28 913.5 18.6 779 15 US-10-440-998-6 Sequence 6, Appl  
29 913 18.6 789 9 US-09-321-801-2 Sequence 2, Appl  
30 913 18.6 789 15 US-10-618-252-2 Sequence 2, Appl  
31 912 18.6 803 15 US-10-440-998-4 Sequence 4, Appl  
32 911.5 18.6 766 15 US-10-440-998-2 Sequence 2, Appl  
33 911.5 18.6 791 9 US-09-321-801-4 Sequence 4, Appl  
34 911.5 18.6 791 15 US-10-618-252-4 Sequence 4, Appl  
35 908 18.5 796 9 US-09-321-801-15 Sequence 15, Appl  
36 908 18.5 796 15 US-10-618-252-15 Sequence 15, Appl  
37 892 18.2 684 14 US-10-168-402-6 Sequence 6, Appl  
38 889 18.1 773 14 US-10-202-107-2 Sequence 2, Appl  
39 889 18.1 773 17 US-10-887-276-2 Sequence 2, Appl  
40 845.5 17.2 576 9 US-09-891-216-13 Sequence 13, Appl  
41 845.5 17.2 576 16 US-10-746-197-3 Sequence 3, Appl  
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43 804 16.4 875 14 US-10-115-515-23 Sequence 23, Appl  
44 804 16.4 875 14 US-10-094-168B-5 Sequence 5, Appl  
45 804 16.4 875 17 US-10-771-833-1 Sequence 1, Appl

#### ALIGNMENTS

RESULT 1  
US-09-883-825-43  
; Sequence 43, Application US/09883825  
; Patent No. US20020151024A1  
; GENERAL INFORMATION:  
; APPLICANT: Beavo, Joseph A.  
; Bentley, Kelley  
; Charbonneau, Harry  
; Sonnenburg, William K.  
; TITLE OF INVENTION: DNA Encoding Mammalian  
; Phosphodiesterases  
; NUMBER OF SEQUENCES: 58  
; CORRESPONDENCE ADDRESS:  
; ADDRESSEE: Marshhall, O'Toole, Gerstein, Murray &  
; STREET: Two First National Plaza, 20 South Clark  
; Street  
; CITY: Chicago  
; STATE: Illinois  
; COUNTRY: USA  
; ZIP: 60603  
; COMPUTER READABLE FORM:  
; MEDIUM TYPE: Floppy disk  
; COMPUTER: IBM PC compatible  
; OPERATING SYSTEM: PC-DOS/MS-DOS  
; SOFTWARE: PatentIn Release #1.0, Version #1.25  
; CURRENT APPLICATION DATA:  
; APPLICATION NUMBER: US/09/883,825  
; FILING DATE: 18-Jun-2001  
; CLASSIFICATION: <Unknown>  
; PRIOR APPLICATION DATA:  
; APPLICATION NUMBER: 09/123,783  
; FILING DATE: <Unknown>  
; APPLICATION NUMBER: 08/297,494

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; FILING DATE: <Unknown>
; APPLICATION NUMBER: US 07/688,356
; FILING DATE: 04-APR-1991
; ATTORNEY/AGENT INFORMATION:
; NAME: No. US20020151024aland, Greta E.
; REGISTRATION NUMBER: 35,302
; REFERENCE/DOCKET NUMBER: 27866/30822
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (312) 346-5750
; TELEFAX: (312) 984-9740
; TELEX: 25-3856
; INFORMATION FOR SEQ ID NO: 43:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 942 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: protein
; SEQUENCE DESCRIPTION: SEQ ID NO: 43:
US-09-883-825-43

Query Match 100.0%; Score 4911; DB 9; Length 942;
Best Local Similarity 100.0%; Pred. No. 0;
Matches 942; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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Db 61 AGLQAAVKEALSAVLPKVETVYTYLLDGSRLVCEEPHELPOBQKREAVISRKLGCN 120
Qy 121 GLGSPDLPKPLARLAPLAPDTQVLPVLDKAGAVAAVILVHCQGLSNEBSLQAV 180
Db 121 GLGSPDLPKPLARLAPLAPDTQVLPVLDKAGAVAAVILVHCQGLSNEBSLQAV 180
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Db 181 EKHTLVAKRVAQLQRESSVAPETQNPPEAAGDQGGVAYTDQRKILQLCGELYDL 240
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Db 241 DASSILQLKVLQYLOQETOASRCCLLVSEDNLQLSCKVIGKVLBEETISFPLTTGRLGQV 300
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;
; FILING DATE: <Unknown>
; APPLICATION NUMBER: US 07/688,356
; FILING DATE: 04-APR-1991
; ATTORNEY/AGENT INFORMATION:
; NAME: No. US20020151024aland, Greta E.
; REGISTRATION NUMBER: 35,302
; REFERENCE/DOCKET NUMBER: 27866/30822
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (312) 346-5750
; TELEFAX: (312) 984-9740
; TELEX: 25-3856
; INFORMATION FOR SEQ ID NO: 43:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 942 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: protein
; SEQUENCE DESCRIPTION: SEQ ID NO: 43:
US-10-697-894-43

Query Match 100.0%; Score 4911; DB 16; Length 942;
Best Local Similarity 100.0%; Pred. No. 0;
Matches 942; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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Db 781 LQKMAEYGYDRTNKQHSHLLCLLMTSCDLSQDTKGWKTTRKIAELIYKEFPFSGDLEKA 840
Qy 841 MGNRPMEHMDREKAYIPELQISFMEHIAMPTIKLQDLFPKAAELYERVAASRREHWTKVS 900
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RESULT 2
US-10-697-894-43
; Sequence 43, Application US/10697894
; Publication No. US20040126866A1
; GENERAL INFORMATION:
; APPLICANT: Beavo, Joseph A.
; Bentley, Kelley
; Charbonneau, Harry
; Sonnenburg, William K.
; TITLE OF INVENTION: DNA Encoding Mammalian
; NUMBER OF SEQUENCES: 58
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Marshall, O'Toole, Gerstein, Murray &
; Bicknell
; STREET: Two First National Plaza, 20 South Clark
; City: Street
; CITY: Chicago
; STATE: Illinois
; COUNTRY: USA
; ZIP: 60603
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patent In Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/10/697,894
; FILING DATE: 30-Oct-2003
; CLASSIFICATION: <Unknown>
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US/09/123,783
; FILING DATE: 28-July-1998
; APPLICATION NUMBER: 08/297,494
; FILING DATE: <Unknown>
; APPLICATION NUMBER: US 07/688,356
; FILING DATE: 04-APR-1991
; ATTORNEY/AGENT INFORMATION:
; NAME: Noland, Greta E.
; REGISTRATION NUMBER: 35,302
; REFERENCE/DOCKET NUMBER: 27866/30822
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (312) 346-5750
; TELEFAX: (312) 984-9740
; TELEX: 25-3856
; INFORMATION FOR SEQ ID NO: 43:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 942 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: protein
; SEQUENCE DESCRIPTION: SEQ ID NO: 43:
US-10-697-894-43

Query Match 100.0%; Score 4911; DB 16; Length 942;
Best Local Similarity 100.0%; Pred. No. 0;
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Db 721 SSEGSMERHHFPAQAIALNTHGCNI FDHFSKDYQRMLDLMDRIILATDLAHLRI FKD 780  
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Db 901 HKFTIRGLPSNNSLDFLDEEVEVPDLDGARAPINGCCSLDAE 942

RESULT 3

US-09-883-825-45  
; Sequence 45, Application US/09883825  
; Patent No. US20020151024A1  
; GENERAL INFORMATION:  
; APPLICANT: Beavo, Joseph A.  
; Bentley, Kelley

Charbonneau, Harry  
Sonnenburg, William K.  
TITLE OF INVENTION: DNA Encoding Mammalian  
Phosphodiesterases  
NUMBER OF SEQUENCES: 58  
CORRESPONDENCE ADDRESS:  
ADDRESSEE: Marshall, O'Toole, Gerstein, Murray &  
Bicknell  
STREET: Two First National Plaza, 20 South Clark  
Street  
CITY: Chicago  
STATE: Illinois  
COUNTRY: USA  
ZIP: 60603  
COMPUTER READABLE FORM:  
MEDIUM TYPE: Floppy disk  
COMPUTER: IBM PC compatible  
OPERATING SYSTEM: PC-DOS/MS-DOS  
SOFTWARE: Patentin Release #1.0, Version #1.25  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/09/883,825  
FILING DATE: 18-Jun-2001  
CLASSIFICATION: <Unknown>  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: 09/123,783  
FILING DATE: <Unknown>  
APPLICATION NUMBER: 08/297,494  
FILING DATE: <Unknown>  
APPLICATION NUMBER: US 07/688,356  
FILING DATE: 04-APR-1991  
ATTORNEY/AGENT INFORMATION:  
NAME: NO. US20020151024A1and, Greta E.  
REGISTRATION NUMBER: 35,302  
REFERENCE/DOCKET NUMBER: 27866/30822  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: (312) 346-5750  
TELEFAX: (312) 984-9740  
TELEX: 25-3856  
INFORMATION FOR SEQ ID NO: 45:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 941 amino acids  
TYPE: amino acid  
TOPOLOGY: linear  
MOLECULE TYPE: protein  
SEQUENCE DESCRIPTION: SEQ ID NO: 45:  
US-09-883-825-45

Query Match 96.3%; Score 4728.5; DB 9; Length 941;  
Best Local Similarity 96.0%; Pred. No. 0;  
Matches 904; Conservative 18; Mismatches 19; Indels 1; Gaps 1;  
Qy 1 MGACGHSILCRSQOYPAAPRPGQOVFLKDPDEPPPPPCADSLQDALLSLGSDIV 60  
Db 1 MGACGHSILCRSQOYPAAPRPGQOVFLKDPDEPPPPPCADSLQDALLSLGSDIV 60  
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Db 181 EKHTLVALKRVQALQOQRESSVAPETQNPPEAAGDQKGVAYTDQDRKILQCGELYDL 240  
Qy 241 DASSLQKLVQLYQOQTOASRCLLVSDNLQSLCKVIGDKVLEBEISFPITTTGRGQV 300  
Db 241 DASSLQKLVQLYQOQTOASRCLLVSDNLQSLCKVIGDKVLEBEISFPITTTGRGQV 300  
Qy 301 VEDKKSILQKDLTSEDMDQOQSLMGLGCEVQAMLCVPVISRATQVVALACAFNKLGGDLFT 360  
Db 301 VEDKKSILQKDLTSEDMDQOQSLMGLGCEVQAMLCVPVISRATQVVALACAFNKLGGDLFT 360





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Db 660 HAFSVSHFCYLLYKNLENTYLEDIEIFALFISCMCHDLDRGTNNSFOVASKSVLAALY 719
Qy 721 SSEGSMERHFAQAIAIINTHGCNIFDHFSKDYQRMILDMRDIIILATDLAHLRIKFD 780
Db 720 SSEGSMERHFAQAIAIINTHGCNIFDHFSKDYQRMILDMRDIIILATDLAHLRIKFD 779
Qy 781 LQKMAEVGYDRNKKOHHSLILCLMTSCDLSQDTGKWKTRKIAELIYKEPFSQGDLEKA 840
Db 780 LQKMAEVGYDRNKKOHHSLILCLMTSCDLSQDTGKWKTRKIAELIYKEPFSQGDLEKA 839
Qy 841 MGNRPMMMDREKAYIPELQISFMEHIAMPIYKLLQDLFPKAAELYERVASNRHWTKVS 900
Db 840 MGNRPMMMDREKAYIPELQISFMEHIAMPIYKLLQDLFPKAAELYERVASNRHWTKVS 899
Qy 901 HKFTIRGLPSNNSLDFLDEEYVPLDGDARAPINGCCSLDAE 942
Db 900 HKFTIRGLPSNNSLDFLDEEYVPLDGDTRAPINGCCSLDAE 941

RESULT 5
US-10-686-390-5
; Sequence 5, Application US/10686390
; Publication No. US20040254153A1
; GENERAL INFORMATION:
; APPLICANT: Pfizer Inc.
; APPLICANT: Pfizer Limited
; APPLICANT: Maw, Graham Nigel
; APPLICANT: Wayman, Christopher Peter
; TITLE OF INVENTION: Compounds for the Treatment of Female Sexual Dysfunction
; FILE REFERENCE: PC10343B
; CURRENT APPLICATION NUMBER: US/10/686,390
; PRIOR FILING DATE: 2003-10-15
; PRIOR APPLICATION NUMBER: US 09/708,392
; PRIOR FILING DATE: 2000-11-08
; PRIOR APPLICATION NUMBER: US 60/175,161
; PRIOR FILING DATE: 2000-03-29
; PRIOR APPLICATION NUMBER: GB 9926437.6
; PRIOR FILING DATE: 1999-11-08
; PRIOR APPLICATION NUMBER: GB 0004021.2
; PRIOR FILING DATE: 2000-02-18
; PRIOR APPLICATION NUMBER: GB 0013001.3
; PRIOR FILING DATE: 2000-05-26
; PRIOR APPLICATION NUMBER: GB 0016563.9
; PRIOR FILING DATE: 2000-07-05
; PRIOR APPLICATION NUMBER: GB 0017141.3
; PRIOR FILING DATE: 2000-07-12
; PRIOR APPLICATION NUMBER: US 60/192,962
; PRIOR FILING DATE: 2000-03-29
; PRIOR APPLICATION NUMBER: US 60/217,479
; PRIOR FILING DATE: 2000-07-11
; PRIOR APPLICATION NUMBER: US 60/221,014
; PRIOR FILING DATE: 2000-07-27
; Remaining Prior Application data removed - See File Wrapper or PALM.
; NUMBER OF SEQ ID NOS: 20
; SOFTWARE: PatentIn version 3.2
; SEQ ID NO 5
; LENGTH: 941
; TYPE: PRT
; ORGANISM: Homo Sapiens
US-10-686-390-5

Query Match 96.3%; Score 4728.5; DB 16; Length 941;
Best Local Similarity 96.0%; Pred. No. 0;
Matches 904; Conservative 18; Mismatches 19; Indels 1; Gaps 1;

Qy 1 MQQACGHILCRSQQYPAARPAERPGQVFLKPDPEPPPPPCADSLQDALLSLGSDIVD 60
Db 1 MQQACGHILCRSQQYPAARPAERPGQVFLKPDPEPPPPPCADSLQDALLSLGSDIVD 60

Qy 61 AGLOQAVKEALSAPLKVETVYVYLLDGSERLVCBEPHPLPQEGKREAVISRKLCGN 120
Db 61 SGLQRAVKEALSAPLKVETVYVYLLDGSERLVCBEPHPLPQEGKREAVISRKLCGN 120
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Qy 121 GLGPSDLPGKPLARLVAPLAPDTQVLVPIPLVDKEAGAAVAVILVHCQQLSDNEWSLQAV 180
Db 121 GLGPSDLPGKPLARLVAPLAPDTQVLVMPPLADKEAGAAVAVILVHCQQLSDNEWSLQAV 180
Qy 181 BXHTTVALKRVQALQORESSVAPETONPPBEAAGDQKGVAVTDDDRKILQLCGLYDL 240
Db 181 BXHTTVALKRVQALQOQRPAPRAVQNPPEGTAEQDQKGAAYTDDRKILQLCGLYDL 240
Qy 241 DASSLQLKVLQYLOQETOQASRCCLLLVSDNLQLSCKVIGDKVLEEEISFPPLTTGRLQGV 300
Db 241 DASSLQLKVLQYLOQETRASRCCLLLVSDNLQLSCKVIGDKVLEEVFPL-TGCLQGV 299
Qy 301 VEDKKSIOQLKOLITSEDMQOLQSMGLCEVQAMLCVPVISRATQOVVALACAFNKLGGDLFT 360
Db 300 VEDKKSIOQLKOLITSEDMQOLQSMGLCEVQAMLCVPVISRATQOVVALACAFNKLGGDLFT 359
Qy 361 DODEHVIQHCPHYTSTVLTSTLAFOKEOKLKECCALLOVAKNLFTHLDDVSVLQEIIT 420
Db 360 DEDEHVIQHCPHYTSTVLTSTLAFOKEOKLKECCALLOVAKNLFTHLDDVSVLQEIIT 419
Qy 421 EARNLSNAEICSVFLLDQNELVAKVFDGGVDESEYRIRIPADQGIAGHATTGQILNIP 480
Db 420 EARNLSNAEICSVFLLDQNELVAKVFDGGVDESEYRIRIPADQGIAGHATTGQILNIP 479
Qy 481 DAYAHPLFYRGVDDSTGFRTRNLCFPIKNENQEVIGVLAELVKNKINGPWFSPDEDLATA 540
Db 480 DAYAHPLFYRGVDDSTGFRTRNLCFPIKNENQEVIGVLAELVKNKINGPWFSPDEDLATA 539
Qy 541 PSIIYCGISIAHSLLYKKYNEAQYRSHLANEMMYHMKVSDDEYTKLLHDGIIQFVAIDSN 600
Db 540 PSIIYCGISIAHSLLYKKYNEAQYRSHLANEMMYHMKVSDDEYTKLLHDGIIQFVAIDSN 599
Qy 601 PASFTYTPRSIPEDDTSMAILSMLQDMNFNNYKIDCPTLARFCLMVKKGYRDPVHNWM 660
Db 600 PASFTYTPRSIPEDDTSMAILSMLQDMNFNNYKIDCPTLARFCLMVKKGYRDPVHNWM 659
Qy 661 HAFSVSHFCYLLYKNLENTYLEDMEIFALFISCMCHDLDRGTNNSFOVASKSVLAALY 720
Db 660 HAFSVSHFCYLLYKNLENTYLEDIEIFALFISCMCHDLDRGTNNSFOVASKSVLAALY 719
Qy 721 SSEGSMERHFAQAIAIINTHGCNIFDHFSKDYQRMILDMRDIIILATDLAHLRIKFD 780
Db 720 SSEGSMERHFAQAIAIINTHGCNIFDHFSKDYQRMILDMRDIIILATDLAHLRIKFD 779
Qy 781 LQKMAEVGYDRNKKOHHSLILCLMTSCDLSQDTGKWKTRKIAELIYKEPFSQGDLEKA 840
Db 780 LQKMAEVGYDRNKKOHHSLILCLMTSCDLSQDTGKWKTRKIAELIYKEPFSQGDLEKA 839
Qy 841 MGNRPMMMDREKAYIPELQISFMEHIAMPIYKLLQDLFPKAAELYERVASNRHWTKVS 900
Db 840 MGNRPMMMDREKAYIPELQISFMEHIAMPIYKLLQDLFPKAAELYERVASNRHWTKVS 899
Qy 901 HKFTIRGLPSNNSLDFLDEEYVPLDGDARAPINGCCSLDAE 942
Db 900 HKFTIRGLPSNNSLDFLDEEYVPLDGDTRAPINGCCSLDAE 941
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## RESULT 6

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US-10-686-282-5
; Sequence 5, Application US/10686282
; Publication No. US20050020547A1
; GENERAL INFORMATION:
; APPLICANT: Pfizer Inc.
; APPLICANT: Pfizer Limited
; APPLICANT: Maw, Graham Nigel
; APPLICANT: Wayman, Christopher Peter
; TITLE OF INVENTION: Compounds for the Treatment of Female Sexual Dysfunction
; FILE REFERENCE: PC10343D
; CURRENT APPLICATION NUMBER: US/10/686,282
; CURRENT FILING DATE: 2003-10-15
; PRIOR APPLICATION NUMBER: US 09/708,392
; PRIOR FILING DATE: 2000-11-08
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; PRIOR APPLICATION NUMBER: US 60/175,161
; PRIOR FILING DATE: 2000-03-29
; PRIOR APPLICATION NUMBER: GB 9926437.6
; PRIOR FILING DATE: 1999-11-08
; PRIOR APPLICATION NUMBER: GB 0004021.2
; PRIOR FILING DATE: 2000-02-18
; PRIOR APPLICATION NUMBER: GB 0013001.3
; PRIOR FILING DATE: 2000-05-26
; PRIOR APPLICATION NUMBER: GB 0016563.9
; PRIOR FILING DATE: 2000-07-05
; PRIOR APPLICATION NUMBER: GB 0017141.3
; PRIOR FILING DATE: 2000-07-12
; PRIOR APPLICATION NUMBER: US 60/192,962
; PRIOR FILING DATE: 2000-03-29
; PRIOR APPLICATION NUMBER: US 60/217,479
; PRIOR FILING DATE: 2000-07-11
; PRIOR APPLICATION NUMBER: US 60/221,014
; PRIOR FILING DATE: 2000-07-27
; Remaining Prior Application data removed - See File Wrapper or PALM.
; NUMBER OF SEQ ID NOS: 20
; SOFTWARE: PatentIn version 3.2
; SEQ ID NO 5
; LENGTH: 941
; TYPE: PRT
; ORGANISM: Homo Sapiens
US-10-686-282-5

Query Match          96.3%; Score 4728.5; DB 17; Length 941;
Best Local Similarity 96.0%; Pred. No. 0;
Matches 904; Conservative 18; Mismatches 19; Indels 1; Gaps 1;

QY 1 MQACGHSILCRSQQYPAARPAERPGQVFLKPDPEPPPPQPCADSLQDALLSLGSDIV 60
DB 1 MQACGHSILCRSQQYPAARPAERPGQVFLKPDPEPPPPQPCADSLQDALLSLGSDIV 60
QY 61 AGLQQAQVKEALSAVLPKVETVTVYLLDGBSRLVCEBPPELPHQEGKREAVISRKLG 120
DB 61 SGLQRAQVKEALSAVLPRVETVTVYLLDGBSRLVCEBPPELPHQEGKREAVISRKLG 120
QY 121 GLGFSDLPGKPLARLVAPLAPDTQVPLVDVKEAGAVAAVILVHCGSLDNEEWSLQAV 180
DB 121 GLGFSDLPGKPLARLVAPLAPDTQVPLVDVKEAGAVAAVILVHCGSLDNEEWSLQAV 180
QY 181 EKHTLVAKRVQALQORESSVAPEATONPPEEAAGDQKGVAYYTDODRKILQLCGELYDL 240
DB 181 EKHTLVAKRVQALQORESSVAPEATONPPEEAAGDQKGVAYYTDODRKILQLCGELYDL 240
QY 241 DASSLQKVLQVLYQBTQASRCLLVSDNQLQSLCKVIGDKVLEEEISFPLTTGRIGQV 300
DB 241 DASSLQKVLQVLYQBTQASRCLLVSDNQLQSLCKVIGDKVLEEEISFPLTTGRIGQV 300
QY 301 VEDKSIQLKDLTSEDVQOQSLMGCEVQAMLQVPIVRATDQVVALACAEFKLGDLFT 360
DB 301 VEDKSIQLKDLTSEDVQOQSLMGCEVQAMLQVPIVRATDQVVALACAEFKLGDLFT 360
QY 361 DQDEHVIQCHFTYISVTLSTLAFQEKQKCECQALLQVAKNLFTHLDDVSVLLQEIIT 420
DB 361 DQDEHVIQCHFTYISVTLSTLAFQEKQKCECQALLQVAKNLFTHLDDVSVLLQEIIT 420
QY 421 EARNLSNAEICSVFLLDQNLVAKVFDGQVDESEYEIRIPADQGIAGHVATTQOILNIP 480
DB 421 EARNLSNAEICSVFLLDQNLVAKVFDGQVDESEYEIRIPADQGIAGHVATTQOILNIP 480
QY 481 DAYAHLPLFRGVDDSTGFRTRNLCPPPIKNEQVIGVLAELVKNKGFWFSKPEDLATA 540
DB 481 DAYAHLPLFRGVDDSTGFRTRNLCPPPIKNEQVIGVLAELVKNKGFWFSKPEDLATA 540
QY 541 FSIYCGISIAHSLYLYKKVNEAQVRSFLANEMMYHKVSDDEYTKLLHDGQIPVAAIDSN 600
DB 541 FSIYCGISIAHSLYLYKKVNEAQVRSFLANEMMYHKVSDDEYTKLLHDGQIPVAAIDSN 600
QY 601 FASFTYTPRSLPEDDTSMAILSMLQDMNFINNYKIDCPTLARFCLMWKKYRPPPPYHNWM 659
DB 601 FASFTYTPRSLPEDDTSMAILSMLQDMNFINNYKIDCPTLARFCLMWKKYRPPPPYHNWM 659

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QY 61 AGLOAVKEALSAVLPKVTETVTVYLLDGSERLVCEPPELHPQEGKREAVISRKLGCN 120
Db :|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
61 SGLQAVKEALSAVLPKVTETVTVYLLDGSERLVCEPPELHPQEGKREAVISRKLGCN 120
QY 121 GLGPSDLPGKPLARLAVAPLAPDQVLPVLDKEAGAAVAVILVHCGQLSDNEEWSLOAV 180
Db :|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
121 GLGPSDLPGKPLARLAVAPLAPDQVLPVLDKEAGAAVAVILVHCGQLSDNEEWSLOAV 180
QY 181 EKHGTLVALKRVQALQOQRESSVAPEATQNPPEAAAGQKGGVAYTDDQDKILQLCGELYDL 240
Db :|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
181 EKHGTLVALKRVQALQOQRESSVAPEATQNPPEAAAGQKGGVAYTDDQDKILQLCGELYDL 240
QY 241 DASSIQLKVLQVLOQETQASRCLLLVSDNQLSKVKVIGDKVLSEETSPFUTTRGLQGV 300
Db :|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
241 DASSIQLKVLQVLOQETQASRCLLLVSDNQLSKVKVIGDKVLSEETSPFUTTRGLQGV 300
QY 301 VEDKKSIOQLKDLTSDMQOQSMGLCEVQAMLCVPIVSRATDOVVALLACAFNKLGGDLFT 360
Db :|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
301 VEDKKSIOQLKDLTSDMQOQSMGLCEVQAMLCVPIVSRATDOVVALLACAFNKLGGDLFT 360
QY 361 DODEHVIQHCFTYTSVLTSTLAFQKEQKLKCECQALLQVAKNLFTHLDDVSVLLQEIIT 420
Db :|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
361 DODEHVIQHCFTYTSVLTSTLAFQKEQKLKCECQALLQVAKNLFTHLDDVSVLLQEIIT 420
QY 421 EARNLSNAEICSVFLLDQNELVAKVDFGQVDESEYIRIPADQGIAGHVATTGQILNIP 480
Db :|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
421 EARNLSNAEICSVFLLDQNELVAKVDFGQVDESEYIRIPADQGIAGHVATTGQILNIP 480
QY 481 DAYAHLPLVGVDDSTGTRNLCFPKINENOEVIGVAELVNKINGPWFSEKFDLATA 540
Db :|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
481 DAYAHLPLVGVDDSTGTRNLCFPKINENOEVIGVAELVNKINGPWFSEKFDLATA 540
QY 541 FSIYCGISIAHSLLYKKYNEAQYRHLANEMMYHMKVSDDEYTKLLHDGQPVAAIDSN 600
Db :|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
541 FSIYCGISIAHSLLYKKYNEAQYRHLANEMMYHMKVSDDEYTKLLHDGQPVAAIDSN 600
QY 601 FASFTYTPRSLPEDDTSMAILSMLQDMFNINNYKIDCPTLARFCLMWKGYRDPYHNMM 660
Db :|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
601 FASFTYTPRSLPEDDTSMAILSMLQDMFNINNYKIDCPTLARFCLMWKGYRDPYHNMM 660
QY 661 HAFSVSHFCYLLYKULELTVNLEDEIIFALPFSCHCHOLDHRTGNTNSFQVASKSVLAALY 720
Db :|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
661 HAFSVSHFCYLLYKULELTVNLEDEIIFALPFSCHCHOLDHRTGNTNSFQVASKSVLAALY 720
QY 721 SSEGVSMEHHPFAQAIILNTHGNCNIFDHFGRKDYQRMLDLMDRIILATDLAHLRIKFD 780
Db :|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
721 SSEGVSMEHHPFAQAIILNTHGNCNIFDHFGRKDYQRMLDLMDRIILATDLAHLRIKFD 780
QY 781 LQKMAEVGYDRTNKOHSLLLCLLMTSCDLSQTKGWKTKRIABELIYKEFFSQGDLEKA 840
Db :|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
781 LQKMAEVGYDRTNKOHSLLLCLLMTSCDLSQTKGWKTKRIABELIYKEFFSQGDLEKA 840
QY 841 MGNRPMEWMDREKAYIPELOISFMEHIANPIYKLLQDLFPKAAELYERVASNREHWTKVS 900
Db :|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
841 MGNRPMEWMDREKAYIPELOISFMEHIANPIYKLLQDLFPKAAELYERVASNREHWTKVS 900
QY 901 HKFTIRGLPNSNSLDLFLDEEVEVPLDGCARAPINGCCSLDAE 942
Db :|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
901 HKFTIRGLPNSNSLDLFLDEEVEVPLDGCARAPINGCCSLDAE 942
QY 900 HKFTIRGLPNSNSLDLFLDEEVEVPLDGTTRAPINGCCSLDAE 941
Db :|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
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## RESULT 8

US-09-883-825-39

; Sequence 39, Application US/09883825

; Patent No. US20020151024A1

; GENERAL INFORMATION:

; APPLICANT: Beavo, Joseph A.

; Bentley, Kelley

; Charbonneau, Harry

; Sonnenburg, William K.

; TITLE OF INVENTION: DNA Encoding Mammalian

; Phosphodiesterases

; NUMBER OF SEQUENCES: 58

```
; CORRESPONDENCE ADDRESS:
; ADDRESSES: Marshall, O'Toole, Gerstein, Murray &
; Bicknell
; STREET: Two First National Plaza, 20 South Clark
; Street
; CITY: Chicago
; STATE: Illinois
; COUNTRY: USA
; ZIP: 60603
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patent In Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/883,825
; FILING DATE: 18-Jun-2001
; CLASSIFICATION: <Unknown>
; PRIOR APPLICATION NUMBER: 09/123,783
; FILING DATE: <Unknown>
; APPLICATION NUMBER: 08/297,494
; FILING DATE: <Unknown>
; APPLICATION NUMBER: US 07/688,356
; FILING DATE: 04-APR-1991
; ATTORNEY/AGENT INFORMATION:
; NAME: NO. US20020151024A1and, Greta E.
; REGISTRATION NUMBER: 35,302
; REFERENCE/DOCKET NUMBER: 27866/30822
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (312) 346-5750
; TELEFAX: (312) 984-9740
; TELEX: 25-3856
; INFORMATION FOR SEQ ID NO: 39:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 921 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: protein
; SEQUENCE DESCRIPTION: SEQ ID NO: 39:
;
; US-09-883-825-39
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Query Match 94.8%; Score 4657; DB 9; Length 921;  
Best Local Similarity 98.9%; Pred. No. 0;  
Matches 898; Conservative 3; Mismatches 7; Indels 0; Gaps 0;

Qy	35	EPPPPPPQCADSLQDALLSLGSDVDVAGLQQAQVKEALSAVLPKVTETVTVYLLDGSERLVC	94
Db	14	QEPVPPGSGDQALQDALLSLGSDVDVAGLQQAQVKEALSAVLPKVTETVTVYLLDGSERLVC	73
Qy	95	BEPPHELPOEGKREAVISRKLGCNGLGSDLPKGLARLAVAPLAPDTQVLVPLVDKE	154
Db	74	BEPPHELPOEGKREAVISRKLGCNGLGSDLPKGLARLAVAPLAPDTQVLVPLVDKE	133
Qy	155	AGAAVAAILVHCGQLSDNEEWSLQAVEKHTLVALKRVQALQOQRESSVAPEATQNPPEAA	214
Db	134	AGAAVAAILVHCGQLSDNEEWSLQAVEKHTLVALKRVQALQOQRESSVAPEATQNPPEAA	193
Qy	215	GDQKGGVAYTDDQDKILQLCGELYDLDAASSLQKLVQLQOQETQASRCLLLVSDNLQ	274
Db	194	GDQKGGVAYTDDQDKILQLCGELYDLDAASSLQKLVQLQOQETQASRCLLLVSDNLQ	253
Qy	275	SKVIGDKVLSEETSPFUTTRGLQGVVEDKKSIOQLKDLTSDMQOQSMGLCEVQAMLCV	334
Db	254	SKVIGDKVLSEETSPFUTTRGLQGVVEDKKSIOQLKDLTSDMQOQSMGLCEVQAMLCV	313
Qy	335	PVISRATDQVVALLACAFNKLGGDLFTDQDEHVIQHCFTYTSVLTSTLAFQKEQKLKCEC	394
Db	314	PVISRATDQVVALLACAFNKLGGDLFTDQDEHVIQHCFTYTSVLTSTLAFQKEQKLKCEC	373
Qy	395	QALLQVAKNLFTHLDDVSVLLQEIITEARNLSNAEICSVFLLDQNELVAKVDFGQVDE	454
Db	374	QALLQVAKNLFTHLDDVSVLLQEIITEARNLSNAEICSVFLLDQNELVAKVDFGQVDE	433

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QY 455 SYEIRIPADQGIAGHVATTGQILNIPDAYAHPLFYRGVDDSTGTRNLCFFIKENOE 514
Db 434 SYEIRIPADQGIAGHVATTGQILNIPDAYAHPLFYRGVDDSTGTRNLCFFIKENOE 493
QY 515 VIGVAELVNKINGPWFSGFDEDLATAFISYICGISHLSLLYKKNVNEAQYRSHLANEMMY 574
Db 494 VIGVAELVNKINGPWFSGFDEDLATAFISYICGISHLSLLYKKNVNEAQYRSHLANEMMY 553
QY 575 HMKVSDDEYTKLLHDGIIQPVAAIDSNFASFTYTPRSLPEDDTSMAILSMLQDMNFINNYK 634
Db 554 HMKVSDDEYTKLLHDGIIQPVAAIDSNFASFTYTPRSLPEDDTSMAILSMLQDMNFINNYK 613
QY 635 IDCPTLAFRCFLMWKGYRDPYPHNMHAFSVSHFCYLLYKNLELTNYLEDMEIFALFISC 694
Db 614 IDCPTLAFRCFLMWKGYRDPYPHNMHAFSVSHFCYLLYKNLELTNYLEDMEIFALFISC 673
QY 695 MCHDLDRGTNNNSFOVASKSVLAALYSSEGSMERHHPAQAIILNTHGNCNIFDHFSRKD 754
Db 674 MCHDLDRGTNNNSFOVASKSVLAALYSSEGSMERHHPAQAIILNTHGNCNIFDHFSRKD 733
QY 755 YQRMDLMDRIILATDLAHLRIFKDLQKMAEVGYDRTNKHSHLLCLLMTSCDLSQDT 814
Db 734 YQRMDLMDRIILATDLAHLRIFKDLQKMAEVGYDRTNKHSHLLCLLMTSCDLSQDT 793
QY 815 KGWTKTRKIAELIYKEFPFSGDLEKAMGNRPWEMMDREKAYIPELOISFMHIAMPIYKL 874
Db 794 KGWTKTRKIAELIYKEFPFSGDLEKAMGNRPWEMMDREKAYIPELOISFMHIAMPIYKL 853
QY 875 LQDLFPKAAELYERVASNRHWTKVSHKFTIRGLPNSNSLDFLDBEYVPLDGDARAPIN 934
Db 854 LQDLFPKAAELYERVASNRHWTKVSHKFTIRGLPNSNSLDFLDBEYVPLDGDARAPIN 913
QY 935 GCCSLDAE 942
Db 914 GCCSLDAE 921

RESULT 9
US-10-094-989-5
; Sequence 5, Application US/10094989
; Publication No. US20020115179A1
; GENERAL INFORMATION:
; APPLICANT: WEI, Ming-Hui et al
; TITLE OF INVENTION: ISOLATED HUMAN PHOSPHODIESTERASE
; TITLE OF INVENTION: PROTEINS, NUCLEIC ACID MOLECULES ENCODING HUMAN
; TITLE OF INVENTION: PHOSPHODIESTERASE PROTEINS, AND USES THEREOF
; FILE REFERENCE: CL001063DIV
; CURRENT APPLICATION NUMBER: US/10/094,989
; CURRENT FILING DATE: 2002-03-12
; PRIOR APPLICATION NUMBER: 09/754,250
; PRIOR FILING DATE: 2001-01-05
; NUMBER OF SEQ ID NOS: 5
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 5
; LENGTH: 921
; TYPE: PRT
; ORGANISM: Bos taurus
US-10-094-989-5

Query Match 94.8%; Score 4657; DB 13; Length 921;
Best Local Similarity 98.9%; Pred. No. 0;
Matches 898; Conservative 3; Mismatches 7; Indels 0; Gaps 0;

QY 35 EPPPPPPQCADSLQDALLSLGSDVIDVAGLQQAQVKEALSAPLKVETVYTYLLDGSRLVC 94
Db 14 QEPVPPGSGDGLQDALLSLGSDVIDVAGLQQAQVKEALSAPLKVETVYTYLLDGSRLVC 73
QY 95 EEPHELPQEGKVRNAVTSRRLGNCGLPGSDLPGLKPLARLVAFLAPDTQVLVPLVDKE 154
Db 74 EEPHELPQEGKVRNAVTSRRLGNCGLPGSDLPGLKPLARLVAFLAPDTQVLVPLVDKE 133
QY 155 AGAAVAATLVHCGQLSDNEEWSLQAVEKHTLVALKRVQALQORESSVAPEATQNPPEAA 214
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Db 134 AGAAVAATLVHCGQLSDNEEWSLQAVEKHTLVALKRVQALQORESSVAPEATQNPPEAA 193
QY 215 GDQKGGVAYTDQDKIILQCGELYDLDAASSLQKLVLYLQOETQASRCLLLVSDNLQOL 274
Db 194 GDQKGGVAYTNQDKRILQCGELYDLDAASSLQKLVLYLQOETQASRCLLLVSDNLQOL 253
QY 275 SKKVIGDKVLVEEETSFPITTCRGLQGVVDEKSIQDKDLTSEDMOOLOSLMCEVQAMLCV 334
Db 254 SKKVIGDKVLVEEETSFPITTCRGLQGVVDEKSIQDKDLTSEDMOOLOSLMCEVQAMLCV 313
QY 335 PVISRATDQVVALACAFNKLGGDLFTDQDEHVIQHCFTYTSVLTSTLAFQEKQLKCEC 394
Db 314 PVISRATDQVVALACAFNKLGGDLFTDQDEHVIQHCFTYTSVLTSTLAFQEKQLKCEC 373
QY 395 QALLQVAKNLFTHLDDVSLLQEIITEARNLSNAEISCVFLDDQNELVAKVDFDGVVDE 454
Db 374 QALLQVAKNLFTHLDDVSLLQEIITEARNLSNAEISCVFLDDQNELVAKVDFDGVVDE 433
QY 455 SYEIRIPADQGIAGHVATTGQILNIPDAYAHPLFYRGVDDSTGTRNLCFFIKENOE 514
Db 434 SYEIRIPADQGIAGHVATTGQILNIPDAYAHPLFYRGVDDSTGTRNLCFFIKENOE 493
QY 515 VIGVAELVNKINGPWFSGFDEDLATAFISYICGISHLSLLYKKNVNEAQYRSHLANEMMY 574
Db 494 VIGVAELVNKINGPWFSGFDEDLATAFISYICGISHLSLLYKKNVNEAQYRSHLANEMMY 553
QY 575 HMKVSDDEYTKLLHDGIIQPVAAIDSNFASFTYTPRSLPEDDTSMAILSMLQDMNFINNYK 634
Db 554 HMKVSDDEYTKLLHDGIIQPVAAIDSNFASFTYTPRSLPEDDTSMAILSMLQDMNFINNYK 613
QY 635 IDCPTLAFRCFLMWKGYRDPYPHNMHAFSVSHFCYLLYKNLELTNYLEDMEIFALFISC 694
Db 614 IDCPTLAFRCFLMWKGYRDPYPHNMHAFSVSHFCYLLYKNLELTNYLEDMEIFALFISC 673
QY 695 MCHDLDRGTNNNSFOVASKSVLAALYSSEGSMERHHPAQAIILNTHGNCNIFDHFSRKD 754
Db 674 MCHDLDRGTNNNSFOVASKSVLAALYSSEGSMERHHPAQAIILNTHGNCNIFDHFSRKD 733
QY 755 YQRMDLMDRIILATDLAHLRIFKDLQKMAEVGYDRTNKHSHLLCLLMTSCDLSQDT 814
Db 734 YQRMDLMDRIILATDLAHLRIFKDLQKMAEVGYDRTNKHSHLLCLLMTSCDLSQDT 793
QY 815 KGWTKTRKIAELIYKEFPFSGDLEKAMGNRPWEMMDREKAYIPELOISFMHIAMPIYKL 874
Db 794 KGWTKTRKIAELIYKEFPFSGDLEKAMGNRPWEMMDREKAYIPELOISFMHIAMPIYKL 853
QY 875 LQDLFPKAAELYERVASNRHWTKVSHKFTIRGLPNSNSLDFLDBEYVPLDGDARAPIN 934
Db 854 LQDLFPKAAELYERVASNRHWTKVSHKFTIRGLPNSNSLDFLDBEYVPLDGDARAPIN 913
QY 935 GCCSLDAE 942
Db 914 GCCSLDAE 921

RESULT 10
US-10-697-894-39
; Sequence 39, Application US/10697894
; Publication No. US20040126866A1
; GENERAL INFORMATION:
; APPLICANT: Beavo, Joseph A.
; Bentley, Kelley
; Charbonneau, Harry
; Sonnenburg, William K.
; TITLE OF INVENTION: DNA Encoding Mammalian
; Phosphodiesterases
; NUMBER OF SEQUENCES: 58
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Marshall, O'Toole, Gerstein, Murray &
; Bicknell
; STREET: Two First National Plaza, 20 South Clark
; Street
```



Db 181 QKGAAYTDRDKILQLCGELYDLASSLQLKVLQYLOQETRASRCCLLLVSDNLQLSC 240  
Qy 277 KVIQDKVLEBISPLTTGRIGQVVEDKKSQTKDLTSEDQOQOSMLGCEVQAMLCVPV 336  
Db 241 KVIQDKVLEBISFPL-TGCLGQVVEDKKSQTKDLTSEDVQOQOSMLGCEVQAMLCVPV 299  
Qy 337 ISRATDQVVALACAFNKLGGDLFTDQDDEHVIQHCFTYSTVLTSTLAFQKQKLCCEQA 396  
Db 300 ISRATDQVVALACAFNKLGGDLFTDQDDEHVIQHCFTYSTVLTSTLAFQKQKLCCEQA 359  
Qy 397 LLQVAKNLFTHLDDVSVLLQBIITEARNLSNAEICSVFLLDQNELVAKVFDGQVVDSEY 456  
Db 360 LLQVAKNLFTHLDDVSVLLQBIITEARNLSNAEICSVFLLDQNELVAKVFDGQVVDSEY 419  
Qy 457 EIRIPADQGIAGHVATTGQIILNIPDAYAHPLFYRGVDDSTGFRTRNIIICFPKIKENQBEVI 516  
Db 420 EIRIPADQGIAGHVATTGQIILNIPDAYAHPLFYRGVDDSTGFRTRNIIICFPKIKENQBEVI 479  
Qy 517 GVAELVNKINGPWFSEKPEDLATAFSIYCGISIAHSLLYKKVNEAQYRSHLANEMMYHM 576  
Db 480 GVAELVNKINGPWFSEKPEDLATAFSIYCGISIAHSLLYKKVNEAQYRSHLANEMMYHM 539  
Qy 577 KVSDEYTKLLHDGQIPVAAIDSNFASFTYTPRSLPEDDTSMALLSMLQDMNFNNYKID 636  
Db 540 KVSDEYTKLLHDGQIPVAAIDSNFASFTYTPRSLPEDDTSMALLSMLQDMNFNNYKID 599  
Qy 637 CPTLARFCLMVKGYRDPYPYHNMHAFSVSHFCVLLYKNLELTYNLEDMETIFALPISCMC 696  
Db 600 CPTLARFCLMVKGYRDPYPYHNMHAFSVSHFCVLLYKNLELTYNLEDMETIFALPISCMC 659  
Qy 756 HDLDRGTNNISFQVASKSVLAALYSSEGSVMERHHFAQIAIALNTHGNCIIFDHFSRKYQ 756  
Db 660 HDLDRGTNNISFQVASKSVLAALYSSEGSVMERHHFAQIAIALNTHGNCIIFDHFSRKYQ 719  
Qy 816 RMLDLMRDIILATDLAHLRIFKDLQKMAEYGVYDRTNKHSHLLCLLMTSCDLSQTKG 816  
Db 720 RMLDLMRDIILATDLAHLRIFKDLQKMAEYGVYDRTNKHSHLLCLLMTSCDLSQTKG 779  
Qy 876 WKTRKIAELIYKEFFSQGDLSEKANGNRPMMMDREKAYIPELQISFMEHTAMPIYKLLQ 876  
Db 780 WKTRKIAELIYKEFFSQGDLSEKANGNRPMMMDREKAYIPELQISFMEHTAMPIYKLLQ 839  
Qy 936 DLFPKAAELYERVANSRHHWTQVSHKFTIRGLPSNNSLDLDEEYEVPLDQARAPINGC 936  
Db 840 DLFPKAAELYERVANSRHHWTQVSHKFTIRGLPSNNSLDLDEEYEVPLDQARAPINGC 899  
Qy 937 CSLDAB 942  
Db 900 CSLDAB 905

## RESULT 12

US-10-236-417-78

; Sequence 78, Application US/10236417

; Publication No. US20040048256A1

; GENERAL INFORMATION:

; APPLICANT: Agee et al.

; TITLE OF INVENTION: NOVEL PROTEINS AND NUCLEIC ACIDS ENCODING SAME

; FILE REFERENCE: 21402-442C

; CURRENT APPLICATION NUMBER: US/10/236,417

; CURRENT FILING DATE: 2003-01-06

; PRIOR APPLICATION NUMBER: US60/318,120

; PRIOR FILING DATE: 2001-09-01

; PRIOR APPLICATION NUMBER: US60/318,430

; PRIOR FILING DATE: 2001-09-10

; PRIOR APPLICATION NUMBER: US60/322,781

; PRIOR FILING DATE: 2001-09-17

; PRIOR APPLICATION NUMBER: US60/318,184

; PRIOR FILING DATE: 2001-09-07

; PRIOR APPLICATION NUMBER: US60/361,663

; PRIOR FILING DATE: 2002-03-05

; PRIOR APPLICATION NUMBER: US60/396,412

; PRIOR FILING DATE: 2002-07-17

; PRIOR APPLICATION NUMBER: US60/322,636  
; PRIOR FILING DATE: 2001-09-17  
; PRIOR APPLICATION NUMBER: US60/322,817  
; PRIOR FILING DATE: 2001-09-17  
; PRIOR APPLICATION NUMBER: US60/322,816  
; PRIOR FILING DATE: 2001-09-17  
; PRIOR APPLICATION NUMBER: US60/323,519  
; PRIOR FILING DATE: 2001-09-19  
; Remaining Prior Application data removed - See File Wrapper or PALM.  
; NUMBER OF SEQ ID NOS: 341  
; SOFTWARE: Custom  
; SEQ ID NO 78  
; LENGTH: 920  
; TYPE: PRT  
; ORGANISM: Homo sapiens  
US-10-236-417-78

Query Match 91.2%; Score 4480.5; DB 15; Length 920;

Best Local Similarity 95.0%; Pred. No. 0;

Matches 861; Conservative 19; Mismatches 25; Indels 1; Gaps 1;

Qy 37 PPPQPCADSLQDALLSLGSDIVAGLQQAQVKEALSAVLPKVTYTYTYLLDGESRLVCEE 96  
Db 16 PGPPGSRDRLEDALLSLGSDIVAGLQQAQVKEALSAVLPKVTYTYTYLLDGESRLVCEE 75  
Qy 97 PPHELPOGKGVREAVISRKRLGCGNLGSPDLPGKPLARLVAPLAPDPTOVLPVLDKEAG 156  
Db 76 PPHELPOGKGVREAVISRKRLGCGNLGSPDLPGKPLARLVAPLAPDPTOVLPVLDKEAG 135  
Qy 157 AVAAVILVHCQQLSDNEEWSLQAVEKHTLVALKRVQALQQRRESSVAPATQNPPEEAAGD 216  
Db 136 AVAAVILVHCQQLSDNEEWSLQAVEKHTLVALKRVQALQQRRESSVAPATQNPPEEAAGD 195  
Qy 217 QKGVVATTQDRKTLQICGELYDLDASSLQIKVLYLOOETOASRCCLLLVSDNLQLSC 276  
Db 196 QKGAAYTDRDKTLQICGELYDLDASSLQIKVLYLOOETOASRCCLLLVSDNLQLSC 255  
Qy 277 KVIQDKVLEBISPLTTGRIGQVVEDKKSQTKDLTSEDQOQOSMLGCEVQAMLCVPV 336  
Db 256 KVIQDKVLEBISFPL-TGCLGQVVEDKKSQTKDLTSEDVQOQOSMLGCEVQAMLCVPV 314  
Qy 337 ISRATDQVVALACAFNKLGGDLFTDQDDEHVIQHCFTYSTVLTSTLAFQKQKLCCEQA 396  
Db 315 ISRATDQVVALACAFNKLGGDLFTDQDDEHVIQHCFTYSTVLTSTLAFQKQKLCCEQA 374  
Qy 397 LLQVAKNLFTHLDDVSVLLQBIITEARNLSNAEICSVFLLDQNELVAKVFDGQVVDSEY 456  
Db 375 LLQVAKNLFTHLDDVSVLLQBIITEARNLSNAEICSVFLLDQNELVAKVFDGQVVDSEY 434  
Qy 457 EIRIPADQGIAGHVATTGQIILNIPDAYAHPLFYRGVDDSTGFRTRNIIICFPKIKENQBEVI 516  
Db 435 EIRIPADQGIAGHVATTGQIILNIPDAYAHPLFYRGVDDSTGFRTRNIIICFPKIKENQBEVI 494  
Qy 517 GVAELVNKINGPWFSEKPEDLATAFSIYCGISIAHSLLYKKVNEAQYRSHLANEMMYHM 576  
Db 495 GVAELVNKINGPWFSEKPEDLATAFSIYCGISIAHSLLYKKVNEAQYRSHLANEMMYHM 554  
Qy 577 KVSDEYTKLLHDGQIPVAAIDSNFASFTYTPRSLPEDDTSMALLSMLQDMNFNNYKID 636  
Db 555 KVSDEYTKLLHDGQIPVAAIDSNFASFTYTPRSLPEDDTSMALLSMLQDMNFNNYKID 614  
Qy 637 CPTLARFCLMVKGYRDPYPYHNMHAFSVSHFCVLLYKNLELTYNLEDMETIFALPISCMC 696  
Db 615 CPTLARFCLMVKGYRDPYPYHNMHAFSVSHFCVLLYKNLELTYNLEDMETIFALPISCMC 674  
Qy 697 HDLDRGTNNISFQVASKSVLAALYSSEGSVMERHHFAQIAIALNTHGNCIIFDHFSRKYQ 756  
Db 675 HDLDRGTNNISFQVASKSVLAALYSSEGSVMERHHFAQIAIALNTHGNCIIFDHFSRKYQ 734  
Qy 757 RMLDLMRDIILATDLAHLRIFKDLQKMAEYGVYDRTNKHSHLLCLLMTSCDLSQTKG 816  
Db 735 RMLDLMRDIILATDLAHLRIFKDLQKMAEYGVYDRTNKHSHLLCLLMTSCDLSQTKG 794

QY 817 WKTTRKIAELIYKEPFSQDLEKAMGNRPMEMMDREKAYIPELOISFMEHIAMPIYKLIQ 876  
DB 795 WKTTRKIAELIYKEPFSQDLEKAMGNRPMEMMDREKAYIPELOISFMEHIAMPIYKLIQ 854  
QY 877 DLFPKAAELYERVAASRHHWTKVSHKFTIRGLPSNNSLDPLDEEYEVDPDLCARAPINGC 936  
DB 855 DLFPKAAELYERVAASRHHWTKVSHKFTIRGLPSNNSLDPLDEEYEVDPDLCARAPINGC 914  
QY 937 CSLDAE 942  
DB 915 CSLDAE 920  
RESULT 13  
US-10-094-989-2  
; Sequence 2, Application US/10094989  
; Publication No. US20020115179A1  
; GENERAL INFORMATION:  
; APPLICANT: WEI, Ming-Hui et al  
; TITLE OF INVENTION: ISOLATED HUMAN PHOSPHODIESTERASE  
; TITLE OF INVENTION: PROTEINS, NUCLEIC ACID MOLECULES ENCODING HUMAN  
; TITLE OF INVENTION: PHOSPHODIESTERASE PROTEINS, AND USES THEREOF  
; FILE REFERENCE: CL001063DIV  
; CURRENT APPLICATION NUMBER: US/10/094,989  
; CURRENT FILING DATE: 2002-03-12  
; PRIOR APPLICATION NUMBER: 09/754,250  
; NUMBER OF SEQ ID NOS: 5  
; SOFTWARE: FastSeq for Windows Version 4.0  
; SEQ ID NO 2  
; LENGTH: 920  
; TYPE: PRT  
; ORGANISM: Homo sapien  
US-10-094-989-2  
Query Match 91.1%; Score 4474.5; DB 13; Length 920;  
Best Local Similarity 94.9%; Pred. No. 0;  
Matches 860; Conservative 19; Mismatches 26; Indels 1; Gaps 1;  
QY 37 PPPQPCCADSLQDALLSLGSLVDVAGLOQAVKEALSAVLPKVETVTVYLLDGSERLVCEE 96  
DB 16 FPGPSRRDRLEDAISLGSVIDISGLQAVKEALSAVLPKVETVTVYLLDGSERLVCEE 75  
QY 97 PPHELPOBQKREAVISRRKRLGCGSLDPLGKGLARLAPLAPDQVLPVPLVKEAG 156  
DB 76 PPHELPOBQKREAVISRRKRLGCGSLDPLGKGLARLAPLAPDQVLPVPLVKEAG 135  
QY 157 AVAAVILVHCGQLSDNEBSLQAVKEKHTLVALKRVQALQOQRESSVAPATQNPPEAAGD 216  
DB 136 AVAAVILVHCGQLSDNEBSLQAVKEKHTLVALKRVQALQOQRESSVAPATQNPPEAAGD 195  
QY 217 QKGGVAYTDQDKILQCGELYDLDAISLQKLVQLOQETOASRCCLLLVSEDLNLQSC 276  
DB 196 QKGGAAVYDRDKILQCGELYDLDAISLQKLVQLOQETASRCCLLLVSEDLNLQSC 255  
QY 277 KVIGKVLBEERISFPLTTGRGQVVEDKKSIOKDLTSEDVQOQSLGCEVQAMLCVPV 336  
DB 256 KVIGKVLBEERISFPLTTGRGQVVEDKKSIOKDLTSEDVQOQSLGCEVQAMLCVPV 314  
QY 337 ISRATDQVVALACAFNKLGGDLFTDQDEHVIQHCFTYTSVLTSTLAFQKQKLCCEQA 396  
DB 315 ISRATDQVVALACAFNKLGGDLFTDQDEHVIQHCFTYTSVLTSTLAFQKQKLCCEQA 374  
QY 397 LLOVAKNLFTHLDDVSVLLQEIITEARNLSNAEICSVFLLDONELVAKVFDGGVDESEY 456  
DB 375 LLOVAKNLFTHLDDVSVLLQEIITEARNLSNAEICSVFLLDONELVAKVFDGGVDESEY 434  
QY 457 EIRIPADQGIAGHVAATGQILNIPAYAHPLPYRGVDDSTGPRTRNIIICFPKIKENQSVI 516  
DB 435 EIRIPADQGIAGHVAATGQILNIPAYAHPLPYRGVDDSTGPRTRNIIICFPKIKENQSVI 494  
QY 517 GVAELVNKINGPWFKDFEDLATAFSIYCGISIAHSLLYKKVNEAQYRSHLANEMMYHM 576

DB 495 GVAELVNKINGPWFKDFEDLATAFSIYCGISIAHSLLYKKVNEAQYRSHLANEMMYHM 554  
QY 577 KVSDDYETKLLHDGIQPVAAIDSNFASFTYTPRSLPEDDTSMALLSMLQDMNFINNYKID 636  
DB 555 KVSDDYETKLLHDGIQPVAAIDSNFASFTYTPRSLPEDDTSMALLSMLQDMNFINNYKID 614  
QY 637 CPTLARFCLMWKKGVRDPPYHNMHAFSVSHFCYLLYKULELTNYLEDMEIHALFISCMC 696  
DB 615 CPTLARFCLMWKKGVRDPPYHNMHAFSVSHFCYLLYKULELTNYLEDMEIHALFISCMC 674  
QY 697 HDLDRGTNNSFOVASKSVLAALYSSEGSVMERHHPAQAIALNTHGNCNIPHPSRDKYQ 756  
DB 675 HDLDRGTNNSFOVASKSVLAALYSSEGSVMERHHPAQAIALNTHGNCNIPHPSRDKYQ 734  
QY 757 RMLDLMRDIIILATDLAHLRIFKDIQKMAEYGVYDRTNKQHSLLLCCLMTSCDLSQTKG 816  
DB 735 RMLDLMRDIIILATDLAHLRIFKDIQKMAEYGVYDRTNKQHSLLLCCLMTSCDLSQTKG 794  
QY 817 WKTTRKIAELIYKEPFSQDLEKAMGNRPMEMMDREKAYIPELOISFMEHIAMPIYKLIQ 876  
DB 795 WKTTRKIAELIYKEPFSQDLEKAMGNRPMEMMDREKAYIPELOISFMEHIAMPIYKLIQ 854  
QY 877 DLFPKAAELYERVAASRHHWTKVSHKFTIRGLPSNNSLDPLDEEYEVDPDLCARAPINGC 936  
DB 855 DLFPKAAELYERVAASRHHWTKVSHKFTIRGLPSNNSLDPLDEEYEVDPDLCARAPINGC 914  
QY 937 CSLDAE 942  
DB 915 CSLDAE 920  
RESULT 14  
US-10-108-260A-2928  
; Sequence 2928, Application US/10108260A  
; Publication No. US20040005560A1  
; GENERAL INFORMATION:  
; APPLICANT: HELIX RESEARCH INSTITUTE  
; TITLE OF INVENTION: NO. US20040005560A1el full length cDNA  
; FILE REFERENCE: H1-A0106  
; CURRENT APPLICATION NUMBER: US/10/108,260A  
; CURRENT FILING DATE: 2002-03-27  
; NUMBER OF SEQ ID NOS: 5458  
; SOFTWARE: Patent In Ver. 2.1  
; SEQ ID NO 2928  
; LENGTH: 950  
; TYPE: PRT  
; ORGANISM: Homo sapiens  
US-10-108-260A-2928  
Query Match 87.0%; Score 4272.5; DB 15; Length 950;  
Best Local Similarity 92.9%; Pred. No. 0;  
Matches 827; Conservative 21; Mismatches 33; Indels 9; Gaps 2;  
QY 1 MGQACGHILCRSOQYPAAR-----PAPRGGQVFLKPDPEPPPPPPPCADSLQDALL 52  
DB 62 VGPSWTHSGASRSSSRSTRRRRRSHAPTACRRGQVFLKPDPEPPPPPPPCADSLQDALL 121  
QY 53 SLGSLVIDVAGLQAVKEALSAVLPKVETVTVYLLDGSERLVCEEPPHELPOBQKREAVI 112  
DB 122 SLGSLVIDISGLQAVKEALSAVLPKVETVTVYLLDGSERLVCEEPPHELPOBQKREAVI 181  
QY 113 SRKRLGCGNGLGPSDLPGKPLARLAPLAPDQVLPVPLVKEAGAAVAVILVHCGQLSDN 172  
DB 182 SQKRLGCGNGLGFSDDLPGKPLARLAPLAPDQVLPVPLVKEAGAAVAVILVHCGQLSDN 241  
QY 173 EWSLQAVKEKHTLVALKRVQALQOQRESSVAPATQNPPEAAGDQKGVAYTDQDKILQ 232  
DB 242 EWSLQAVKEKHTLVALKRVQALQOQRESSVAPATQNPPEAAGDQKGVAYTDQDKILQ 301  
QY 233 LCGELYDLDAISLQKLVQLOQETOASRCCLLLVSEDLNLQSCVKYIGDKVLEESIPPL 292  
DB 302 LCGELYDLDAISLQKLVQLOQETASRCCLLLVSEDLNLQSCVKYIGDKVLEESIPPL 361

293	Qy	TTGRLGQVVEBKKSITQLKDLTSEDNQOQLQSMLGCEVQAMLCVPVITSRATDQVVALACAPN	352
362	Db	-TGCILQGVVEBKKSITQLKDLTSEDVQOQLQSMGCEIQAMLCVPVITSRATDQVVALACAPN	420
353	Qy	KLGGDLFTDQDEHVIQHCFHYTSTVLTSTLAFQKEOKLCECOALLQVAKNLPHTLDDVS	412
421	Db	KLGGDLFTDQDEHVIQHCFHYTSTVLTSTLAFQKEOKLCECOALLQVAKNLPHTLDDVS	480
413	Qy	VLLQEIITEARNLSNAEICSVFLLDQNELVAKVFDGGVVDESSYEIRIPADOGIAGHVAT	472
481	Db	VLLQEIITEARNLSNAEICSVFLLDQNELVAKVFDGGVVDESSYEIRIPADOGIAGHVAT	540
473	Qy	TGQILNIPDAVAHPLFYKGVDDSTGFRTRNIIICFPPIKNEHQVIGVABELVNKINGPWSK	532
541	Db	TGQILNIPDAVAHPLFYKGVDDSTGFRTRNIIICFPPIKNEHQVIGVABELVNKINGPWSK	600
533	Qy	FDEDLATAFSIYCGISIAHSLLYKKVNEAQVYRSHLANEMMYHMKVSDDEYTKLHDGIGQ	592
601	Db	FDEDLATAFSIYCGISIAHSLLYKKVNEAQVYRSHLANEMMYHMKVSDDEYTKLHDGIGQ	660
593	Qy	PVAIDSNFASFYTYPRSLPEDDTSMAILSMLQDMNFNNYKIDCPTLARFCMLVKKGYR	652
661	Db	PVAIDSNFASFYTYPRSLPEDDTSMAILSMLQDMNFNNYKIDCPTLARFCMLVKKGYR	720
653	Qy	DPVYHNMWAFSVSHFCYLLYKNLELTNYLEDMEIFALFISCMCHDLHRGTNNNSFQVAS	712
721	Db	DPVYHNMWAFSVSHFCYLLYKNLELTNYLEDIEIFALFISCMCHDLHRGTNNNSFQVAS	780
713	Qy	KSVLAALYSSGGSVMERHHFAQAIALNTHGCNI EDHFSRKDYQRMULD MRDII IATDLA	772
781	Db	KSVLAALYSSGGSVMERHHFAQAIALNTHGCNI EDHFSRKDYQRMULD MRDII IATDLA	840
773	Qy	HLHRI FKDLQKMAEYGVDRYTNKQHSLLLCILMTSCDLSDOTKGWKTTRKIAELIYKEFF	832
841	Db	HLHRI FKDLQKMAEYGVDRYTNKQHSLLLCILMTSCDLSDOTKGWKTTRKIAELIYKEFF	900
833	Qy	SQGDLEKANGNRPMEIMDREKAYITPELOISPMHEIAMPIYKLLQDLFPKA	882
901	Db	SQGDLEKANGNRPMEIMDREKAYITPELOISPMHEIAMPIYKLLQDLFPKA	950

RESULT 15

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US-10-104-047-2944
; Sequence 2944, Application US/10104047
; Publication No. US20030236392A1
; GENERAL INFORMATION:
; APPLICANT: HELIX RESEARCH INSTITUTE
; TITLE OF INVENTION: NO. US20030236392A1el full length cDNA
; FILE REFERENCE: H1-A0105
; CURRENT APPLICATION NUMBER: US/10/104,047
; CURRENT FILING DATE: 2002-03-25
; PRIOR APPLICATION NUMBER:
; PRIOR FILING DATE:
; NUMBER OF SEQ ID NOS: 4096
; SOFTWARE: PatentIn ver. 2.1
; SEQ ID NO 2944
; LENGTH: 786
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-104-047-2944

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	Query Match	71.0%; Score 3484.5; DB 15; Length 786;
	Best Local Similarity	94.1%; Pred. No. 7e-274;
	Matches	672; Conservative 19; Mismatches 22; Indels 1; Gaps 1;
Qy	37 PPPQPCCADSLQDALLSGSVSDVAGLQQAVKEALSAVLPKVTYTYLLDGESRLVCEE	96
	:           :           :           :	
	:           :           :           :	
Db	16 PGPGSRDDRLEDALLSGSVSDISGLQRAVKEALSAVLPRTVYTYLLDGESQLVCED	75
	:           :           :           :	
	:           :           :           :	
Qy	97 PPHELPOEGKKREAVISRKLGCNGLGSPDLPGPLARLVAPLDPTQVLVPLVDKEAG	156
	:           :           :           :	
	:           :           :           :	
Db	76 PPHELPOEGKKREAVIISOKRLGCNGLGSPDLPGPLARLVAPLDPTQVLVWPLADKEAG	135
	:           :           :           :	
	:           :           :           :	

Qy	157	AVA	VIL	VHC	Q	S	N	E	W	S	I	L	A	V	E	K	T	L	V	A	K	R	V	Q	A	L	Q	O	R	E	S	S	V	A	P	E	A	A	G	216				
Db	136	AVA	VIL	VHC	Q	S	N	E	W	S	I	L	A	V	E	K	T	L	V	A	K	R	V	Q	A	L	Q	O	R	E	S	S	V	A	P	E	A	A	G	195				
Qy	217	QK	G	V	A	T	D	O	R	K	I	L	Q	C	G	E	L	Y	D	L	D	A	S	I	L	Q	K	V	L	O	Q	E	T	O	A	S	R	C	L	L	276			
Db	196	QK	G	A	A	Y	T	D	R	K	I	L	Q	C	G	E	L	Y	D	L	D	A	S	I	L	Q	K	V	L	O	Q	E	T	R	A	S	R	C	L	L	255			
Qy	277	K	V	I	G	D	K	V	L	E	E	B	I	S	P	P	L	T	G	R	L	G	V	V	E	D	K	S	I	Q	L	K	D	L	T	S	E	D	M	O	Q	L	336	
Db	256	K	V	I	G	D	K	V	L	E	E	B	I	S	P	P	L	-	T	G	C	L	G	V	V	E	D	K	S	I	Q	L	K	D	L	T	S	E	D	V	Q	L	314	
Qy	337	I	S	R	A	T	D	Q	V	A	L	A	C	A	F	N	K	L	G	D	L	F	T	D	D	E	H	V	I	Q	H	C	F	H	Y	T	S	T	L	T	S	L	396	
Db	315	I	S	R	A	T	D	Q	V	A	L	A	C	A	F	N	K	L	E	G	D	L	F	T	D	E	D	E	H	V	I	Q	H	C	F	H	Y	T	S	T	L	T	374	
Qy	397	L	L	O	V	A	K	N	L	F	T	H	D	D	V	S	V	L	Q	E	I	I	T	E	A	R	N	L	S	N	A	E	I	C	S	V	F	L	L	D	O	N	456	
Db	375	L	L	O	V	A	K	N	L	F	T	H	D	D	V	S	V	L	Q	E	I	I	T	E	A	R	N	L	S	N	A	E	I	C	S	V	F	L	L	D	O	N	434	
Qy	457	E	I	R	P	A	D	O	G	I	A	G	H	V	A	T	T	Q	O	I	L	N	I	P	D	A	Y	A	H	P	L	F	Y	R	G	V	D	S	T	G	F	R	N	516
Db	435	E	I	R	P	A	D	O	G	I	A	G	H	V	A	T	T	Q	O	I	L	N	I	P	D	A	Y	A	H	P	L	F	Y	R	G	V	D	S	T	G	F	R	N	494
Qy	517	G	V	A	E	L	V	N	K	I	N	G	P	W	S	K	P	D	E	L	A	T	A	P	S	I	V	C	G	I	S	I	A	H	S	L	L	Y	K	K	V	N	576	
Db	495	G	V	A	E	L	V	N	K	I	N	G	P	W	S	K	P	D	E	L	A	T	A	P	S	I	V	C	G	I	S	I	A	H	S	L	L	Y	K	K	V	N	554	
Qy	577	K	V	S	D	E	Y	T	K	L	A	H	D	G	I	O	P	V	A	A	I	D	S	N	P	A	S	T	T	P	R	S	I	P	E	D	D	T	S	M	A	I	L	636
Db	555	K	V	S	D	E	Y	T	K	L	A	H	D	G	I	O	P	V	A	A	I	D	S	N	P	A	S	T	T	P	R	S	I	P	E	D	D	T	S	M	A	I	L	614
Qy	637	C	P	T	L	A	R	F	C	M	V	K	G	Y	R	D	P	P	P	Y	H	N	M	H	A	F	S	V	S	H	F	C	Y	L	L	Y	K	N	L	E	T	N	696	
Db	615	C	P	T	L	A	R	F	C	M	V	K	G	Y	R	D	P	P	P	Y	H	N	M	H																				

Search completed: June 26, 2005, 12:41:01  
Job time : 120.308 secs